

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2003, 10:17:16 ; Search time 44 Seconds
(without alignments)
415.126 Million cell updates/sec

Title: US-09-990-874-16

Perfect score: 1045

Sequence: 1 QTIQPGTGYNNGYFYWYND.....YQIVAVEGYFSSGSASITVS 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1045	100.0	222	2 S39154	xylanase 1 - fungu
2	1045	100.0	223	2 S39883	endo-1,4-beta-xyla
3	1022	97.8	190	1 A44594	endo-1,4-beta-xyla
4	1005	96.2	190	1 A44595	endo-1,4-beta-xyla
5	996	95.3	190	1 A44593	endo-1,4-beta-xyla
6	765.5	73.3	241	2 S71473	endo-1,4-beta-xyla
7	705.5	67.5	219	2 S71472	endo-1,4-beta-xyla
8	701.5	67.1	232	2 JC7577	endo-1,4-beta-xyla
9	684.5	65.5	225	1 S57477	endo-1,4-beta-xyla
10	670.5	64.2	221	1 S57469	endo-1,4-beta-xyla
11	656	62.8	221	2 JC7307	endo-1,4-beta-xyla
12	614.5	58.8	227	2 S43919	endo-1,4-beta-xyla
13	591	56.6	333	1 JS0590	endo-1,4-beta-xyla
14	591	56.6	335	2 T50601	endo-1,4-beta-xyla
15	575.5	55.1	644	1 I40712	endo-1,4-beta-xyla
16	565.5	54.1	197	1 A44597	endo-1,4-beta-xyla
17	536.5	51.3	661	1 S59633	endo-1,4-beta-xyla
18	530.5	50.8	241	2 T37005	endo-1,4-beta-xyla
19	527	50.4	240	1 JS0591	endo-1,4-beta-xyla
20	526.5	50.4	656	1 S59631	endo-1,4-beta-xyla
21	525	50.2	240	1 S47512	endo-1,4-beta-xyla
22	524.5	50.2	210	2 C83762	endo-1,4-beta-xyla
23	503	48.1	213	1 I40369	endo-1,4-beta-xyla
24	502	48.0	213	1 S01734	endo-1,4-beta-xyla
25	502	48.0	213	1 S48126	endo-1,4-beta-xyla
26	468	44.8	354	1 S51779	endo-1,4-beta-xyla
27	462	44.2	228	1 WWSXP	endo-1,4-beta-xyla
28	453.5	43.4	261	1 SI2745	endo-1,4-beta-xyla
29	444	42.5	511	1 JQ1935	endo-1,4-beta-xyla

xylanase 2 - fungu
endo-1,4-beta-xyla
endo-1,4-beta-xyla
endo-1,4-beta-xyla
endo-1,4-beta-xyla
endo-1,4-beta-xyla
endo-1,4-beta-xyla
xylanase, beta(1,3)
xynB precursor - R
xynB precursor - R
endo-1,4-beta-xyla
endo-1,4-beta-xyla
xylanase (EC 3.2.1
endo-1,4-beta-xyla
endo-1,4-beta-xyla
probable pPE prote
uncharacterized pr

ALIGNMENTS

RESULT 1

S39154

xylanase 1 - fungus (Trichoderma reesei)

C:Species: Trichoderma reesei

C:Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 22-Jun-1999

C:Accession: S39154

R:Toerrien, A.; Mach, R.L.; Messner, R.; Gonzalez, R.; Kalkkinen, N.; Harkki, A.; K

Biotechnology 10, 1461-1465, 1992

A:Title: The two major xylanases from trichoderma reesei: characterization of both en

A:Reference number: S39154

A:Accession: S39154

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-222 <TO>

A:Cross-references: EMBL:X69573; NID:g396563; PIDN:CAA49293.1; >ID:g396564

C:Genetics:

A:Gene: xyl

A:Introns: 90/2

C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

F:44-222/Domain: endo-1,4-beta-xylanase homology <XYL>

Query Match 100.0%; Score 1045; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 7.2e-73;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QTIQPGTGYNNGYFYWYNDGCHGGVYTNPGGQFVNNNSGNGFVGGKGPCTKKNVI 60

Db 33 QTIQPGTGYNNGYFYWYNDGCHGGVYTNPGGQFVNNNSGNGFVGGKGPCTKKNVI 92

Qy 61 NFSGSNPNNGNSYLSVYGSWRNPLIEYIVENFGTNPSTGATKLGEVTSQSVYDIYRT 120

Db 93 NFSGSNPNNGNSYLSVYGSWRNPLIEYIVENFGTNPSTGATKLGEVTSQSVYDIYRT 152

Qy 121 QRVNQPSTIGTATPYQVWYVNRNHRSSGVSNTANHFNAWAQGLTLPMDYQIVAVEGYF 180

Db 153 QRVNQPSTIGTATPYQVWYVNRNHRSSGVSNTANHFNAWAQGLTLPMDYQIVAVEGYF 212

Qy 181 SSGSASITVS 190

Db 213 SSGSASITVS 222

RESULT 2

S39883

endo-1,4-beta-xylanase (EC 3.2.1.8) II precursor - fungus (Trichoderma reesei)

N:Alternate names: endoxylanase II

C:Species: Trichoderma reesei

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 22-Jun-1999

C:Accession: S39883; S39884

R:Saarelainen, R.; Paloneimo, M.; Fagerstrom, R.; Suominen, P.L.; Nevalainen, K.M.H.

Mol. Gen. Genet. 241, 497-503, 1993

A:Title: Cloning, sequencing and enhanced expression of the Trichoderma reesei endoxy

A:Reference number: S39883; MUID:94088442; PMID:8264524

A:Accession: S39883

A:Molecule type: DNA

A:Residues: 1-223 <SAA>

A:Cross-references: EMBL:S67387; NID:9455906; PIDN:AAB29346.1; PID:9455907

A:Experimental source: strain QM6a

A:Accession: S39884

A:Molecule type: protein

A:Residues: 34-43;49-57;121-151;178-191 <SAF>

C:Genetics:

A:Gene: xln2

A:Introns: 91/2

C:Function:

A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans

A:Pathway: xylan degradation

C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-33/Domain: propeptide #status predicted <PRO>

F:34-223/Product: endo-1,4-beta-xylanase II #status experimental <MAT>

F:45-223/Domain: endo-1,4-beta-xylanase homology <XYL>

F:71,94/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:110,121/Binding site: substrate (Tyr) #status predicted

F:119,210/Active site: Glu #status predicted

Query Match 100.0%; Score 1045; DB 2; Length 223;

Best Local Similarity 100.0%; Pred. No. 7.2e-73;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTIGPGTGNGCYFYSYWNDGHHGVYTTNGPGQFQSVNNSGNGFVGGKQWPGTKNKVI 60

Db 34 QTIGPGTGNGCYFYSYWNDGHHGVYTTNGPGQFQSVNNSGNGFVGGKQWPGTKNKVI 93

QY 61 NFSGSYNPNGNSYLSYVWGRNPLIEYIVENFGTNPSTGATKLGCVTS DGSVDIYRT 120

Db 94 NFSGSYNPNGNSYLSYVWGRNPLIEYIVENFGTNPSTGATKLGCVTS DGSVDIYRT 153

QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTLGTM DYQIVAVEGYF 180

Db 154 QRVNPSIIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTLGTM DYQIVAVEGYF 213

QY 181 SSGSASITVS 190

Db 214 SSGSASITVS 223

RESULT 3

A44594

endo-1,4-beta-xylanase (EC 3.2.1.8) IIA - fungus (Trichoderma viride)

N:Alternate names: xylanase IIA

C:Species: Trichoderma viride

C:Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 07-Nov-1997

C:Accession: A44594

R:Yaguchi, M.

submitted to the Protein Sequence Database, March 1994

A:Reference number: A44593

A:Molecule type: protein

A:Residues: 1-190 <YAG>

C:Function:

A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans

A:Pathway: xylan degradation

C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

C:Keywords: glycosidase; hydrolase; polysaccharide degradation

F:12-190/Domain: endo-1,4-beta-xylanase homology <XYL>

F:77,88/Binding site: substrate (Tyr) #status predicted

F:86,177/Active site: Glu #status predicted

Query Match

Best Local Similarity 97.8%; Score 1022; DB 1; Length 190;

Matches 185; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QTIGPGTGNGCYFYSYWNDGHHGVYTTNGPGQFQSVNNSGNGFVGGKQWPGTKNKVI 50

Db 1 QTIGPGTGNGCYFYSYWNDGHHGVYTTNGPGQFQSVNNSGNGFVGGKQWPGTKNKVI 60

QY 61 NFSGSYNPNGNSYLSYVWGRNPLIEYIVENFGTNPSTGATKLGCVTS DGSVDIYRT 120

Db 61 NFSGSYNPNGNSYLSYVWGRNPLIEYIVENFGTNPSTGATKLGCVTS DGSVDIYRT 120

QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTLGTM DYQIVAVEGYF 180

Db 121 QRVNPSIIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTLGTM DYQIVAVEGYF 180

QY 181 SSGSASITVS 190

Db 181 SSGSASITVS 190

RESULT 4

A44595

endo-1,4-beta-xylanase (EC 3.2.1.8) IIB (proteinase-sensitive) - fungus (Trichoderma

N:Alternate names: xylanase IIB

C:Species: Trichoderma viride

C:Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 13-Mar-1998

C:Accession: A44595

R:Yaguchi, M.

submitted to the Protein Sequence Database, March 1994

A:Reference number: A44593

A:Accession: A44595

A:Molecule type: protein

A:Residues: 1-190 <YAG>

C:Function:

A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans

A:Pathway: xylan degradation

C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

C:Keywords: glycosidase; hydrolase; polysaccharide degradation

F:12-190/Domain: endo-1,4-beta-xylanase homology <XYL>

F:86,177/Active site: Glu #status predicted

F:126-127/Cleavage site: Pro-Ser (unidentified proteinase) #status predicted

F:129-130/Cleavage site: Glu-Gly (unidentified proteinase) #status predicted

Query Match 96.2%; Score 1005; DB 1; Length 190;

Best Local Similarity 95.8%; Pred. No. 6.8e-70;

Matches 182; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIGPGTGNGCYFYSYWNDGHHGVYTTNGPGQFQSVNNSGNGFVGGKQWPGTKNKVI 60

Db 1 QTIGPGTGNGCYFYSYWNDGHHGVYTTNGPGQFQSVNNSGNGFVGGKQWPGTKNKVI 60

QY 61 NFSGSYNPNGNSYLSYVWGRNPLIEYIVENFGTNPSTGATKLGCVTS DGSVDIYRT 120

Db 61 NFSGSYNPNGNSYLSYVWGRNPLIEYIVENFGTNPSTGATKLGCVTS DGSVDIYRT 120

QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTLGTM DYQIVAVEGYF 180

Db 121 QRVNPSIIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTLGTM DYQIVAVEGYF 180

QY 181 SSGSASITVS 190

Db 181 SSGSASITVS 190

RESULT 5

A44593

endo-1,4-beta-xylanase (EC 3.2.1.8) [validated] - fungus (Trichoderma harzianum) (str

N:Alternate names: xylanase

C:Species: Trichoderma harzianum

C:Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 15-Sep-2000

C:Accession: A44593

R:Yaguchi, M.

submitted to the Protein Sequence Database, March 1994

A:Reference number: A44593

A:Accession: A44593

A:Molecule type: protein


```

QY      127  SIIGTATFYQYWSVRRNHRSSGVSTANTANHENAWAQOGLTLGTM DYQYVAVEGYFSSGSSAS 186
      || ||||| |:|||||:: |:|:| ||||| ||| |:|:| ||||| ||| |||||
Db      162  SIEGTATFEQFWSVRSQKRTGGTVTANTANHENAWAALGMRLGTHNYQYIVATGEGYQSSGSSAS 221

QY      187  ITV 189
      |||
Db      222  ITV 224

RESULT 10
S57469
endo-1,4-beta-xylanase (EC 3.2.1.8) 2 precursor - Emericella nidulans
N:Alternate names: xylanase 2
C:Species: Emericella nidulans, Aspergillus nidulans
C:Date: 10-Oct-1995 #sequence_revision 22-Nov-1996 #text_change 08-May-1999

```

[illegible]

N:Alternate names: endo-1,3-beta-xylanase; xylanase
C:Species: *Penicillium* sp.
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C:Accession: JCT307; PC7086
R:Kimura, T.; Ito, J.; Kawano, A.; Makino, T.; Kondo, H.; Karita, S.; Sakka
Biosci. Biotechnol. Biochem. 64, 1230-1237, 2000
A:Title: Purification, characterization, and molecular cloning of acidophi
A:Reference number: JCT307
A:Accession: JCT307
A:Molecule type: DNA
A:Residues: 1-221 <KIN>
A:Cross-references: DDBJ:AB035540

5
4
3
2
1
1
1
0
0
0

C; Genetics:

Search completed: May 9, 2003, 10:21:30
Job time : 45 secs

A:Gene: xlnB
C:Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolase

Query Match 56.6%; Score 591; DB 2; Length 335;
Best Local Similarity 55.1%; Pred. NO. 5.3e-38;
Matches 109; Conservative 31; Mismatches 42; Indels 16; Gaps 5;

QY 5 PGT-----GYNNGYFYSYNDGHHGGVYTTNGPGQFVSNWSNMGVGGKGMQ 52
DB 36 PGTAQADTVTTTNOEGTNGYYSFWDGQTVSMNMGSGGYSTSRNTGNFVACKGWA 95
QY 53 PGTKNKNVFNPSNGSYNSVYGSRNPLIEYIVENFGYNYNSTGATKLGVEYTSOG 112
DB 96 NGR-RTVOYSGSFNPSNAYLALYGTSTNPLVEYIVDNMGTYRP-TGEYK-GTYSOG 152
QY 113 SVYDIYRTORVNOPTIGATFYQYWSVRNRHRSNGSVNTANFNHNAWAOGLTGLTMD-Y 171
DB 153 GTYDIYKTRVNPVSVEGTRTFDQYWSVQAKRTGTTTGNHFDARAGMPLGNFSY 212
QY 172 QIVAVEGYFSSGSASITV 189
DB 213 MINATEGYQSSGSSINV 230

RESULT 15

I40712
endo-1,4-beta-xylanase (EC 3.2.1.8) D precursor - Cellulomonas fimi
N:Alternate names: xylanase D
C:Species: Cellulomonas fimi
C>Date: 16-Aug-1996 #sequence_revision 22-Nov-1996 #text_change 18-Jun-1999
C:Accession: I40712
R:Millward-Sadler, S.J.; Poole, D.M.; Henrissat, B.; Hazlewood, G.P.; Clarke, J.H.; Gilb
Mol. Microbiol. 11, 375-382, 1994
A:Title: Evidence for a general role for high-affinity non-catalytic cellulose binding d
A:Reference number: I40712; MUID:94224155; PMID:8170399
A:Accession: I40712
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-644 <RES>
A:Cross-references: EMBL:X76729; NID:g558176; PIDN:CAA54145.1; PID:g558177
C:Genetics:
A:Gene: xynD
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: Cellulomonas endo-1,4-beta-xylanase D; endo-1,4-beta-xylanase homology;
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-35/Domain: signal sequence #status predicted <SIG>
F:36-644/Product: endo-1,4-beta-xylanase D #status predicted <WAT>
F:34-229/Domain: endo-1,4-beta-xylanase homology <XYL>
F:361-508/Domain: nodB homology <NODB>
F:126,216/Active site: Glu #status predicted

Query Match 55.1%; Score 575.5; DB 1; Length 644;
Best Local Similarity 55.7%; Pred. NO. 1.7e-36;
Matches 103; Conservative 39; Mismatches 38; Indels 5; Gaps 4;

QY 7 TGYNNGYFYSYNDGHHGGVYTTNGPGQFVSNWSNMGVGGKGMQPGTKKNKVINFSGSY 66
DB 49 TGTHDGYFYSFWDSPGSVMDLNSGGYT-RMSNTGNFVACKGWTGGR-KTVSYSGQF 106
QY 67 NPNGNSVLSVYGWSRNPLIEYIVENFGYNYNSTGATKLGVEYTSOGSVYDIYRTORVNOP 126
DB 107 NPSRNAYLTLYGWTSPLVEYIVDSWGYRPT--GTFMGTVTSDGTYDIYRTQVKNP 164
QY 127 SIIG-TATFYQYWSVRNRHRSNGSVNTANFNHNAWAOGLTGLTMDYQIVAVEGYFSSGSA 185
DB 165 STEGDSSTFYQYWSVQKRTGTTTSGNHFDARAGMPLGNFSY 212
QY 186 SITVS 190
DB 225 SITVS 229

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2003, 10:11:31 ; Search time 51 Seconds
(without alignments)
342.841 Million cell updates/sec

Title: US-09-990-874-16

Perfect score: 1045

Sequence: 1 QTIQPGTGYNGFYSYWND.....YQIVAVEGYFSSGSASITVS 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 349150 seqs, 92025710 residues

Total number of hits satisfying chosen parameters: 349150

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	685	65.6	313	9	US-10-213-990-72
2	675.5	64.6	234	9	US-10-213-990-69
3	669.5	64.1	221	9	US-10-213-990-66
4	647	61.9	217	9	US-09-790-070A-11
5	635.5	60.8	225	9	US-09-467-368-2
6	595.5	57.0	344	10	US-09-770-621-2
7	481.5	46.1	133	9	US-09-790-070A-10
8	470	45.0	221	10	US-09-909-207-3
9	470	45.0	248	10	US-09-909-207-6
10	433	41.4	185	9	US-09-970-616-2
11	177	16.9	84	9	US-09-790-070A-9
12	107.5	10.3	943	9	US-09-996-634-131
13	107.5	10.3	943	9	US-09-997-181-131
14	107.5	10.3	943	9	US-09-997-182-131
15	105	10.0	251	9	US-09-880-748-1554
16	103	9.9	250	9	US-09-880-748-1632
17	92.5	8.9	251	9	US-09-880-748-1185
18	92.5	8.9	255	9	US-09-880-748-841
19	89.5	8.6	256	9	US-09-880-748-1607

20	89	8.5	250	9	US-09-880-748-883	Sequence 883, Ap
21	89	8.5	251	9	US-09-880-748-1512	Sequence 1512, Ap
22	88.5	8.5	253	9	US-09-880-748-1339	Sequence 1339, Ap
23	88.5	8.5	254	9	US-09-880-748-1087	Sequence 1087, Ap
24	88.5	8.5	1109	9	US-09-291-417-88	Sequence 88, Appl
25	88	8.4	218	10	US-09-925-300-1671	Sequence 1671, Ap
26	88	8.4	256	9	US-09-880-748-1285	Sequence 1285, Ap
27	88	8.4	353	9	US-09-935-642-14	Sequence 14, Appl
28	87.5	8.4	477	10	US-09-815-242-13881	Sequence 13881, A
29	87	8.3	251	9	US-09-880-748-1562	Sequence 1562, Ap
30	87	8.3	251	9	US-09-880-748-1586	Sequence 1586, Ap
31	87	8.3	251	9	US-09-880-748-1736	Sequence 1736, Ap
32	87	8.3	251	9	US-09-880-748-1869	Sequence 1869, Ap
33	87	8.3	251	9	US-09-880-748-1870	Sequence 1870, Ap
34	87	8.3	251	9	US-09-880-748-1872	Sequence 1872, Ap
35	87	8.3	251	9	US-09-880-748-1878	Sequence 1878, Ap
36	87	8.3	441	9	US-09-916-494A-10	Sequence 10, Appl
37	86.5	8.3	249	9	US-09-880-748-1618	Sequence 1618, Ap
38	86.5	8.3	378	10	US-09-849-967A-2	Sequence 2, Appl
39	86.5	8.3	479	10	US-09-815-242-10288	Sequence 10288, A
40	86.5	8.3	729	10	US-09-815-242-10132	Sequence 10132, A
41	86	8.2	452	1	US-08-841-636A-35	Sequence 35, Appl
42	85.5	8.2	354	9	US-09-820-843A-21	Sequence 21, Appl
43	85.5	8.2	878	10	US-09-912-020-364	Sequence 364, App
44	85	8.1	333	9	US-10-059-261-61	Sequence 61, Appl
45	84.5	8.1	252	9	US-09-880-748-1690	Sequence 1690, Ap

ALIGNMENTS

RESULT 1
US-10-213-990-72
; Sequence 72, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUNIGATUS ENCODING INDUSTRIAL
; TITLE OF INVENTION: ENZYMES AND METHODS OF USE
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Aspergillus
US-10-213-990-72

Query Match	65.6%	Score	685	DB	9	Length	313
Best Local Similarity	64.2%	Pred. No.	2.6e-53				
Matches	124	Conservative	29	Mismatches	36	Indels	4
Gaps							3
Qy	1	QTIQPG-TGYNNGYFYSYWNDGHGVTYTNPGQGFVSNMS--NSGNFVGSGHQPGTKN	57				
Db	32	QTITTSQTGTYNGYFYFWNGAGSVQYTNAGAGEYSVTWANONGDFTCGKGNPGSDH	91				
Qy	58	KVINFGSYNPNGNSYSVYGVWSNRNPLIEYIVENFTYNPSTGATKLGVTSDGVSVDI	117				
Db	92	D-ITFGSGFSPNGNAYLSVYGVWTTNPLVEYILENYGSPNGSGMTHTGTFTSGSTYDI	150				
Qy	118	YRTQVNPQSLTGATATYQYVWSVRNHRSSCSVNTANFNAAOGLTCTMDYQIVAVE	177				
Db	151	YEQOVNPQSLVGTATNQYWSIKQNRKSSGTVTTANHFKAWSLGMNLGTHNTYQIVSTE	210				
Qy	178	GYFSSGSASITVS	190				
Db	211	GYESSGTSITVS	223				

RESULT 2

US-10-213-990-69
; Sequence 69, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Aspergillus
US-10-213-990-69

Query Match 64.6%; Score 675.5; DB 9; Length 234;
Best Local Similarity 63.3%; Pred. No. 1.3e-52;
Matches 119; Conservative 25; Mismatches 39; Indels 5; Gaps 1;
QY 7 TGYNNGYFYSYNDGHHGGVYTTNGPGQFVSVMNSGNEFVGKGMQPGTK-----NKVIN 61
DB 46 TCWNNGYFYSEFTDGGDVTYINGAGGSYSVMNRNVGNEFVGKGNPNPGSARYALSRITIN 105
QY 62 FGSYNPNNSLSYVGSWRNPLIEYYIVENFGTNPSTGATKLGVEVTSVGSDYDIYRTQ 121
DB 106 YGGSFNPNGSLAVYGTWTTNPLIEYYVYESYCTYNPNGSGTFRGTVDGTYNYITAV 165
QY 122 RYNOPSIICTATFYQWSVRNRHRSRGSVTANHFNAWAQOGLTLGTMDYQIVAVEGYES 181
DB 166 RYNAPISIEGKTFTQIWSVRTSKRTGVTMANHFNAWSRLGMLGTHNYQIVATEGYOS 225
QY 182 SGSASITV 189
DB 226 SGSASITV 233

RESULT 3

US-10-213-990-66
; Sequence 66, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Aspergillus
US-10-213-990-66

Query Match 64.1%; Score 669.5; DB 9; Length 221;
Best Local Similarity 64.1%; Pred. No. 4.2e-52;
Matches 118; Conservative 27; Mismatches 38; Indels 1; Gaps 1;
QY 7 TGYNNGYFYSYNDGHHGGVYTTNGPGQFVSVMNSGNEFVGKGMQPGTKNKNVFNFSGY 66
DB 39 TGTNNGYFYSEFTDGGQVYTTNGGQYQVDNNGCNFVACKGNPASE-KAVTYSGSW, 97

QY 67 NPNGNSYLSVYGWSRNPILIEYYIVENFGTNPSTGATKLGVEVTSVGSDYDIYRTQVRNP 126
DB 98 QTSNGYLSVYGWTTSPFLVEFVIVESYGSYDPSGTGATHLCVTESDGTATNLYKTRTNAP 157
QY 127 SIIGTATFYQWSVRNRHRSRGSVTANHFNAWAQOGLTLGTMDYQIVAVEGYESSGSAS 186
DB 158 SIIGTATFYQWSVRTSHRQSGTVTYTKNHFDAWRNAGLQLGNFDMIVATEGYQSSGSAT 217
QY 187 ITVS 190
DB 218 ITVS 221

RESULT 4

US-09-790-070A-11
; Sequence 11, Application US/09790070A
; Publication No. US2003005399A1
; GENERAL INFORMATION:
; APPLICANT: Jonniaux, Jean-Luc
; APPLICANT: Dauvin, Thierry
; TITLE OF INVENTION: ENZYME WITH XYLANASE ACTIVITY
; FILE REFERENCE: VANM199.001AUS
; CURRENT APPLICATION NUMBER: US/09/790,070A
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: EP 00870028.8
; PRIOR FILING DATE: 2000-02-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Penicillium griseofulvum
US-09-790-070A-11

Query Match 61.9%; Score 647; DB 9; Length 217;
Best Local Similarity 63.6%; Pred. No. 4.1e-50;
Matches 117; Conservative 26; Mismatches 39; Indels 2; Gaps 2;

QY 8 GYNNGYFYSYNDGHHGGVYTTNGPGQFVSVMNSGNEFVGKGMQPGTKNKNVFNFSGSYN 67
DB 35 GTNGGYFYSEFTDGGVSVYNNAGNAGQYSVMNKNCSFTSGKGMATGSARN-INP:SGNFEN 93
QY 68 PNGNSYLSVYGWSRNPILIEYYIVENFGTNPSTGATKLGVEVTSVGSDYDIYRTQVRNP 127
DB 94 PSGNAYLAVYGTWTKGPLVEYYIMENYGEYNPGSMTFKGTVTSVGSDYDIYKHTQVNP 153
QY 128 IIG-TATFYQWSVRNRHRSRGSVTANHFNAWAQOGLTLGTMDYQIVAVEGYESSGSAS 186
DB 154 IISDSFTFYQWSIRKNRSGTGTGNTGNHFNWAKLGMGLGSHDYQIVWTEGYQSSGSAT 213
QY 187 ITVS 190
DB 214 ITVS 217

RESULT 5

US-09-467-368-2
; Sequence 2, Application US/09467368
; Patent No. US20020160080A1
; GENERAL INFORMATION:
; APPLICANT: Hansen, Peter Kamp
; APPLICANT: Wagner, Peter
; APPLICANT: Mullertz, Anette
; APPLICANT: Knapp, Inge Helmer
; TITLE OF INVENTION: Animal Feed Additives
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. US20020160080A1
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA


```

;
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/467,368
; FILING DATE: 21-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/886,765
; FILING DATE: 1-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4324.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-467-368-2

```

```

Query Match 60.88; Score 635.5; DB 9; Length 225;
Best Local Similarity 60.28; Pred. No. 4.5e-49;
Matches 115; Conservative 28; Mismatches 47; Indels 1; Gaps 1;

QY 1 QTIQGTGNGYFYSYNDGCHGVYTNPGGQFVSNWSNSGNFVGKGWPGTKNKVI 60
Db 32 QTTNSEGWDGYYYSNWSGGAQATYNLEGGTYEISWGDGNGLVGKGWNPGLNARAI 91

QY 61 NFSGSYPNGNSYLSVYGWSRNPLIEYIYVENFGTYNPSTGATKLGVEYSDGVDIYRT 120
Db 92 HFEGVYQNGNSYLVAVYGTWRNPLVEYIYVENFGTYNPSTGATKLGVEYSDGVDIYRT 151

QY 121 QRVNPSLIGTATFYQYWSVRRNRHSSGSVNTANHFNAWAOQGLT-CTMDYQIVAVEGY 179
Db 152 TRVWPSIDGQTDFQIWSVRQDARTSGTVTGCHFDARAGLVNVDHYQIVAVEGY 211

QY 180 FSSGSASITVS 190
Db 212 FSSGYARITVA 222

```

```

RESULT 6
US-09-770-621-2
; Sequence 2, Application US/09770621
; Patent No. US20010024815A1
; GENERAL INFORMATION:
; APPLICANT: M ntyl, Arja
; APPLICANT: Vehmaanper, Jari
; APPLICANT: Fagerstr m, Richard
; APPLICANT: Lantto, Raija
; APPLICANT: Paloheimo, Marja
; APPLICANT: Suominen, Pirkko
; APPLICANT: Lahtinen, Tarja
; TITLE OF INVENTION: Production and Secretion of Proteins of
; CORRESPONDENCE ADDRESSES: 39
; ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N.W. Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

```

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/770,621
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/590,563
; FILING DATE:
; CLASSIFICATION:
; APPLICATION NUMBER: US 08/332,412
; FILING DATE: 31-OCT-1994
; CLASSIFICATION:
; APPLICATION NUMBER: US 08/282,001
; FILING DATE: 29-JUL-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugalsky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 1050.0340003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-770-621-2

```

```

Query Match 57.0%; Score 595.5; DB 10; Length 344;
Best Local Similarity 56.1%; Pred. No. 2.6e-45;
Matches 105; Conservative 35; Mismatches 44; Indels 3; Gaps 3;

QY 4 QPGTGYNGYFYSYNDGCHGVYTNPGGQFVSNWSNSGNFVGKGWPGTKNKVINFS 63
Db 49 QNQTQDNGYFYSPWTDAPGTVSMTLHSGGSYSTSWRNTGNFVAGKMGSTGGR-RTVTYN 107

QY 64 GSNPNNSYLSVYGWSRNPLIEYIYVENFGTYNPSTGATKLGVEYSDGVDIYRTQRY 123
Db 108 ASFNPSNGYLYLGYWRNPLVEYIYVESWGTYP-RTYK-GTVTDDGGYDIYETWRY 165

QY 124 NPSIIGTATFYQYWSVRRNRHSSGSVNTANHFNAWAOQGLT-CTMDYQIVAVEGYFSSG 183
Db 166 NAPSIEGTRTFQFPWSVRQOKRTSGTITIGNHFDARAGNLSGHDYQINATEGYOSSG 225

QY 184 SASITVS 190
Db 226 SSTVSIS 232

```

```

RESULT 7
US-09-790-070A-10
; Sequence 10, Application US/09790070A
; Publication No. US20030053999A1
; GENERAL INFORMATION:
; APPLICANT: Jonniaux, Jean-Luc
; APPLICANT: Dauvin, Thierry
; TITLE OF INVENTION: ENZYME WITH XYLANASE ACTIVITY
; FILE REFERENCE: VANMI99.001AUS
; CURRENT APPLICATION NUMBER: US/09/790,070A
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: EP 00870028.8
; PRIOR FILING DATE: 2000-02-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 133
; TYPE: PRT

```



```

; TYPE: PKT
; ORGANISM: Homo sapiens
US-09-880-748-1554

Query Match 10.0% Score 105; DB 9; Length 251;
Best Local Similarity 23.4%; Pred. No. 0.067;
Matches 34; Conservative 21; Mismatches 42; Indels

QY 7 TGYNNGYFYSYVNDG-----HGGVTVYTN-----pCG
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```


THIS PAGE BLANK (USPTO)

GenCore version 5.1.4_p5_4578
 Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2003, 10:15:41 ; Search time 30 Seconds
 (without alignments)
 1304.965 Million cell updates/sec

Title: US-09-990-874-16

Perfect score: 1045

Sequence: 1 QTIQPGTGYNGGYFYSYWND.....YQIVAVEGYFSGSASITVS 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1045	100.0	223	3	Q02244
2	1033	98.9	223	3	Q99015
3	876	83.8	223	3	Q9UVF9
4	765.5	73.3	241	3	Q12580
5	705.5	67.5	219	3	Q12579
6	701.5	67.1	232	3	Q9HFA4
7	696.5	66.7	290	3	Q9HEZ0
8	686.5	66.7	290	3	Q9HEY9
9	686.5	65.7	295	3	Q9CLR2
10	680.5	65.1	227	3	Q00263
11	678.5	64.9	227	3	Q9UVZ3
12	665.5	63.7	225	3	Q8TG22
13	656	62.8	221	3	Q9UQ02
14	647.5	62.0	223	3	Q9HFR0
15	635.5	60.8	231	3	Q13447
16	632.5	60.5	346	2	Q8VUT4

ALIGNMENTS

RESULT 1

ID	Q02244	PRELIMINARY;	PRT;	223 AA.
AC	Q02244;			
DT	01-NOV-1996 (TrEMBLrel. 01, Created)			
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)			
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)			
DE	Endoxylanase II.			
GN	XLN2.			
OS	Trichoderma reesei (Hypocrea jecorina).			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;			
OC	Hypocreales; Hypocreaceae; Hypocrea.			
OX	NCBI_TaxID=51453;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94088442; PubMed=8264524;			
RA	Saarelainen R., Paloheimo M., Fagerstrom R., Suominen P.L.,			
RA	Nevalainen K.M.;			
RT	"Cloning, sequencing and enhanced expression of the Trichoderma reesei endoxylanase II (pr 9) gene xln2.";			
RL	Mol. Gen. Genet. 241:497-503(1993).			
DR	EMBL; S67387; AAB29346.1; -			
DR	HSSP; P36217; 1XYO.			
DR	InterPro; IPR001137; GH11.			
DR	Pfam; PF00457; Glyco_hydro.11; 1.			
DR	PRINTS; PR00911; GLYDRLASE1.			
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_Fil_1; 1.			
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_Fil_2; 1.			
KW	Glycosidase; Hydrolase; Xylan degradation.			
SQ	SEQUENCE 223 AA; 24069 MW; 75668149EADA22F9 CRC64;			

Query Match 100.0%; Score 1045; DB 3; Length 223;

Best Local Similarity 100.0%; Pred. No. 7.4e-68;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QTIQPGTGYNGGYFYSYWNDGGGVYTYTNGPGQFSVWNSGNGFVGKGQPGGTFKNKI 60

Db 34 QTIQPGTGYNGGYFYSYWNDGGGVYTYTNGPGQFSVWNSGNGFVGKGQPGGTFKNKI 93

P87037 aspergillus
 Q00350 cochlidiobolus
 P81536 paecilomyces
 Q9hgl humicola gr
 Q96uv7 lentinula e
 Q08346 streptomyces
 Q9rmu4 streptomyces
 Q9rq88 cellulomona
 Q56265 thermomonas
 Q5clr1 fusarium ox
 Q59962 streptomyces
 Q4716 claviceps p
 Q9rmh9 streptomyces
 Q9w89 streptomyces
 Q59674 pseudomonas
 Q9ri72 streptomyces
 Q52375 caldicellul
 Q59300 cellvibrrio
 Q56013 streptomyces
 P7853 dictyoglomu
 Q8vp72 pseudomonas
 Q43993 aeromonas p
 Q8vvc3 bacillus sp
 Q9zb36 bacillus su
 Q59251 bacillus su
 Q59256 bacillus sp
 Q97403 phaenococ

```
QY 61 NFSGSYNPNNGNSYLSYVWNSRNPGLIEYIVENFGTYNPSTGATKLGCVTSKGWQPGTKNKVI 120
DB 94 NFSGSYNPNNGNSYLSYVWNSRNPGLIEYIVENFGTYNPSTGATKLGCVTSKGWQPGTKNKVI 153
QY 121 QRVNQPSSIIGTATFYQYWSVRRNRHSSGVSNTANHFNAWAQOGLTLGTMDYQIVAVEGYF 180
DB 154 QRVNQPSSIIGTATFYQYWSVRRNRHSSGVSNTANHFNAWAQOGLTLGTMDYQIVAVEGYF 213
QY 181 SSGSASITVS 190
DB 214 SSGSASITVS 223

RESULT 2
Q99015
ID Q99015 PRELIMINARY; PRT; 223 AA.
AC Q99015;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Beta-xylanase precursor.
GN XYN2
OS Trichoderma reesei (Hypocrea jecorina).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Hypocreaceae; Hypocrea.
OX NCBI_TaxID=51453;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OM 6A;
RX MEDLINE=97076932; PubMed=8975597;
RA la Grange D.C., Pretorius I.S., van Zyl W.H.;
RT "Expression of a Trichoderma reesei beta-xylanase gene (XYN2) in
RT Saccharomyces cerevisiae."
RL Appl. Environ. Microbiol. 62:1036-1044 (1996).
DR EMBL; U24191; AAB50278.1;
DR HSSP; P36217; LXVO.
DR InterPro; IPR001137; GH_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR GLYcosidase; Hydrolase; Signal; Xylan degradation.
FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 223 BETA-XYLANASE.
SQ SEQUENCE 223 AA; 23981 MW; F696E545DAC90EB4 CRC64;

Query Match 98.9%; Score 1033; DB 3; Length 223;
Best Local Similarity 98.9%; Pred. No. 5.4e-67;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QTPQGTGYNNGYFYSYWNDHGCVTYTNGPGQFVSNNNSNGFVGGKQWPGTKNKVI 60
DB 34 QTPQGTGYNNGYFYSYWNDHGCVTYTNGPGQFVSNNNSNGFVGGKQWPGTKNKVI 93
QY 61 NFSGSYNPNNGNSYLSYVWNSRNPGLIEYIVENFGTYNPSTGATKLGCVTSKGWQPGTKNKVI 120
DB 94 NFSGSYNPNNGNSYLSYVWNSRNPGLIEYIVENFGTYNPSTGATKLGCVTSKGWQPGTKNKVI 153
QY 121 QRVNQPSSIIGTATFYQYWSVRRNRHSSGVSNTANHFNAWAQOGLTLGTMDYQIVAVEGYF 180
DB 154 QRVNQPSSIIGTATFYQYWSVRRNRHSSGVSNTANHFNAWAQOGLTLGTMDYQIVAVEGYF 213
QY 181 SSGSASITVS 190
DB 214 SSGSASITVS 223

RESULT 3
Q9UVF9
ID Q9UVF9 PRELIMINARY; PRT; 223 AA.
AC Q9UVF9;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
```

```
DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8).
OS Trichoderma viride.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; mitosporic Hypocreales; Trichoderma.
OX NCBI_TaxID=5547;
RN [1]
RP SEQUENCE FROM N.A.
RA Furman-Matarasso N., Cohen E., Avni A.;
RT "Mutations in the Active Site of the Ethylene Inducing Xylanase
RT Elicitor Inhibits the b-1-4-Endoxylanase Activity But Not the
RT Elicitation Activity."
RL Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ012718; CAB60757.1;
DR HSSP; P48793; 1XND.
DR InterPro; IPR001137; GH_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR GLYcosidase; Hydrolase; Signal; Xylan degradation.
FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 223 ENDO-1,4-BETA-XYLANASE.
SQ SEQUENCE 223 AA; 24230 MW; FB812028FB1212A CRC64;

Query Match 83.8%; Score 876; DB 3; Length 223;
Best Local Similarity 82.1%; Pred. No. 1e-55;
Matches 156; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

QY 1 QTPQGTGYNNGYFYSYWNDHGCVTYTNGPGQFVSNNNSNGFVGGKQWPGTKNKVI 60
DB 34 QTPQGTGYNNGYFYSYWNDHGCVTYTNGAGGFSVNNNSNGFVGGKQWPNPSSRVI 93
QY 61 NFSGSYNPNNGNSYLSYVWNSRNPGLIEYIVENFGTYNPSTGATKLGCVTSKGWQPGTKNKVI 120
DB 94 NFSGSYNPNNGNSYLSYVWNSRNPGLIEYIVENFGTYNPSTGATKLGCVTSKGWQPGTKNKVI 153
QY 121 QRVNQPSSIIGTATFYQYWSVRRNRHSSGVSNTANHFNAWAQOGLTLGTMDYQIVAVEGYF 180
DB 154 QRVNQPSSIIGTATFYQYWSVRRNRHSSGVSNTANHFNAWAQOGLTLGTMDYQIVAVEGYF 213
QY 181 SSGSASITVS 190
DB 214 SSGSASITVS 223

RESULT 4
Q12580
ID Q12580 PRELIMINARY; PRT; 241 AA.
AC Q12580;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Endo-beta1,4-xylanase (EC 3.2.1.8).
GN CGXB.
OS Chaetomium gracile.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Chaetomiaceae; Chaetomium.
OX NCBI_TaxID=47794;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96118924; PubMed=8595661;
RA Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;
RT "Two family G xylanase genes from Chaetomium gracile and their
RT expression in Aspergillus nidulans."
RL Curr. Genet. 29:73-80 (1995).
DR EMBL; D49851; BAA08650.1;
DR HSSP; P36217; LXVO.
DR InterPro; IPR001137; GH_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR GLYcosidase; Hydrolase; Xylan degradation.
SQ SEQUENCE 241 AA; 25564 MW; DCD4B012272F77F CRC64;
```


Query Match 73.3%; Score 765.5; DB 3; Length 241;
 Best Local Similarity 73.8%; Pred. No. 9.8e-48;
 Matches 135; Conservative 21; Mismatches 26; Indels 1; Gaps 1;

Qy 7 TGYNNGYYSYTWNDGCGVTTNGPGGQFSVNMNSGNFVGGKGPOTKKNKVNFSGSY 66
 Db 38 TGTNNGYYSFTWTDGQGNVYTNAGQGYSVTNGNGNMGVGGKGNPGSA-RTINYTANY 96

Qy 67 NPNGNSYLSVVGWSRNPLEYIYVENFCTYNPSTGATKLGVTSDGSYDIYRTORVNQP 126
 Db 97 NPNGNSYLSVVGWSRNPLEYIYVENFCTYNPSTGATKLGVTSDGSYDIYRTORVNQP 156

Qy 127 SIIGTATFYQWSVRRNHRSSGVSNTANHFNAWAQOGLTGTMDYQIIVAVEGYSSGSAS 186
 Db 157 SIEGTSTFYQWSVRRNHRSSGVSNTANHFNAWAQOGLTGTMDYQIIVAVEGYSSGSAT 216

Qy 187 ITV 189
 Db 217 VNV 219

RESULT 5
 Q12579 PRELIMINARY; PRT; 219 AA.

AC Q12579;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Endo-beta1,4-xylanase A (EC 3.2.1.8).
 GN CGXA.
 OS Chaetomium gracile.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariata; Chaetomiaceae; Chaetomium.
 OX NCBI_TaxID=47794;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96118924; PubMed=8595661;
 RA Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;
 RT "Two family G xylanase genes from Chaetomium gracile and their
 expression in Aspergillus nidulans";
 RL Curr. Genet. 29:73-80(1995).
 DR EMBL; D49850; BAA08649.1; -;
 DR HSSP; P36217; 1XVO.
 DR InterPro; IPR001137; GH_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDRASE11.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Glycosidase; Hydrolase; Xylan degradation.
 SQ SEQUENCE 219 AA; 23324 MW; 4729299E08FD9FBA CRC64;

Query Match 67.5%; Score 705.5; DB 3; Length 219;
 Best Local Similarity 68.1%; Pred. No. 1.8e-43;
 Matches 126; Conservative 23; Mismatches 35; Indels 1; Gaps 1;

Qy 6 GTGNNGYYSYTWNDGCGVTTNGPGGQFSVNMNSGNFVGGKGPOTKKNKVNFSGS 65
 Db 36 GTGNNGYYSYTWNDGCGVTTNGPGGQFSVNMNSGNFVGGKGPOTKKNKVNFSGS 94

Qy 66 YNPNGNSYLSVVGWSRNPLEYIYVENFCTYNPSTGATKLGVTSDGSYDIYRTORVNQ 125
 Db 95 FSPQNGYLSVVGWSRNPLEYIYVENFCTYNPSTGATKLGVTSDGSYDIYRTORVNQ 154

Qy 126 PSIICTATFYQWSVRRNHRSSGVSNTANHFNAWAQOGLTGTMDYQIIVAVEGYSSGSAS 185
 Db 155 PSIEGTSTFYQWSVRRNHRSSGVSNTANHFNAWAQOGLTGTMDYQIIVAVEGYSSGS 214

Qy 186 SITVS 190
 Db 215 SITVS 219

RESULT 6

Q9HEFA4 PRELIMINARY; PRT; 232 AA.

AC Q9HEFA4;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Xylanase G2 (EC 3.2.1.8).
 GN XNG2.
 OS Aspergillus oryzae.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5062;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kimura T., Sakka K., Ohmiya K.;
 RT "Molecular cloning, overexpression, and purification of major xylanase
 from Aspergillus oryzae";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB044941; BAB20794.1; -;
 DR HSSP; P36217; 1XVO.
 DR InterPro; IPR001137; GH_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDRASE11.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Glycosidase; Hydrolase.
 SQ SEQUENCE 232 AA; 24605 MW; 1F73104751EA561C CRC64;

Query Match 67.1%; Score 701.5; DB 3; Length 232;
 Best Local Similarity 67.8%; Pred. No. 3.7e-43;
 Matches 124; Conservative 25; Mismatches 33; Indels 1; Gaps 1;

Qy 7 TGYNNGYYSYTWNDGCGVTTNGPGGQFSVNMNSGNFVGGKGPOTKKNKVNFSGSY 66
 Db 50 TGYNNGYYSYTWNDGCGVTTNGPGGQFSVNMNSGNFVGGKGPOTKKNKVNFSGSY 108

Qy 67 NPNGNSYLSVVGWSRNPLEYIYVENFCTYNPSTGATKLGVTSDGSYDIYRTORVNQP 126
 Db 109 NPNGNSYLSVVGWSRNPLEYIYVENFCTYNPSTGATKLGVTSDGSYDIYRTORVNQP 168

Qy 127 SIIGTATFYQWSVRRNHRSSGVSNTANHFNAWAQOGLTGTMDYQIIVAVEGYSSGSAS 186
 Db 169 SIIGTATFYQWSVRRNHRSSGVSNTANHFNAWAQOGLTGTMDYQIIVAVEGYSSGSAS 228

Qy 187 ITV 189
 Db 229 ITV 231

RESULT 7
 Q9HEZ0 PRELIMINARY; PRT; 290 AA.

AC Q9HEZ0;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Endo-1,4-B-xylanase B.
 GN XNB.
 OS Phanerochaete chrysosporium.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Aphyllophorales; Corticiaceae; Phanerochaete.
 OX NCBI_TaxID=5306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ME446;
 RA Khan S.N., Loera-Corral O., Aspinall T.V., Sims P.F.G.;
 RT "Molecular characterization and expression analysis of two endo-1,4-B-
 xylanase genes from Phanerochaete chrysosporium";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF301904; AAG44994.1; -;
 DR HSSP; P00725; IAZ6.
 DR InterPro; IPR000254; CBD_fungal.


```

OC mitosporic Pezizomycotina; Ascomycota.
OX NCBI_TaxID=47971;
RN [1]
RP SEQUENCE FROM N.A.
RA Lubeck P.S., Paulin L., Degefu Y., Lubeck M., Collinge D.;
RT "Molecular cloning and DNA sequencing of a xylanase gene from the
RL phytopathogenic fungus Ascochyta pisi Lib.;"
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z68891; CAA93120.1; -
DR HSSP: O43097; LYNA.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Signal; Xylan degradation.
FT SIGNAL 19.
FT CHAIN 19.
SQ SEQUENCE 227 AA; 24010 MW; 692AE1FAE035CF0F CRC64;

Query Match 65.1%; Score 680.5; DB 3; Length 227;
Best Local Similarity 65.3%; Pred. No. 1.2e-41;
Matches 126; Conservative 22; Mismatches 40; Indels 5; Gaps 2;

Qy 2 TIQPGT----CYNNGYFYSYWNDCGGVYTYNGPGQFSVNWNSGNFVGKGNPGTKN 57
Db 34 TARAGTPSSQGTGNGCFYSWMTDGGAAQATYTNAGAGSYSVNMTGCGNLVGGKGNPGAA- 92
Qy 58 KVINFSGYNGNSYLSVYGWSRNPLIEYIVENFGTYNPGTGTATKLGVEYTSFGSVYDI 117
Db 93 RTIYSGTYSFGNSYLAVGWRNPLIEYIVVENFGTYDPSSQNTYKGVGTADSSVYKI 152
Qy 118 YRTQVNPQSIIGTATFYQYWSVRNRHRSRSGSVNTANHFNAWAOOGLTLGTMDOYI 177
Db 153 AQTORTNPQSIDGRTQFOQYWSVRQNRSSGVNMTKTFDAWASKMNLGSHYQIVATEGYF 215
Qy 178 GFSSGSASITVS 190
Db 213 GFSSGSASITVN 225

RESULT 11
Q9UV23 ID Q9UV23 PRELIMINARY; PRT; 227 AA.
AC Q9UV23;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Xylanase precursor.
GN XYL1.
OS Helminthosporium turcicum.
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Helminthosporium.
OX NCBI_TaxID=93612;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=H2;
RC Degefu Y., Paulin L., Peraenen J., Lubeck P.S.;
RT "Cloning, sequencing and expression of a xylanase gene from the maize
RL pathogen Helminthosporium turcicum Pass.;"
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ238895; CAB52417.1; -
DR HSSP: O43097; LYNA.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Signal.
FT SIGNAL 19.
FT CHAIN 20.
FT CHAIN 20.
SQ SEQUENCE 227 AA; 24123 MW; BA86FC075EE5306E CRC64;

Query Match 64.9%; Score 678.5; DB 3; Length 227;
Best Local Similarity 64.7%; Pred. No. 1.6e-41;

```

```

Matches 123; Conservative 23; Mismatches 43; Indels 1; Gaps 1;
Qy 1 OTIQPGTGYNNGYFYSYWNDCGGVYTYNGPGQFSVNWNSGNFVGKGNPGTKNVI 60
Db 37 QSTPNGEHTHNGCFYSWMSDGGARATYNGAGGSYSVSWGTGGLVGGKGNPGTA-RTI 95
Qy 61 NFSGYNPNGNSYLSVYGWSRNPLIEYIVENFGTYNPGTGTATKLGVEYTSFGSVYDIYRT 120
Db 96 TYSQYNPNGNSYLSYLAIGWRNPLIEYIVVENFGTYDPSSQAQNGTIVTSFGSSVYKIAQS 155
Qy 121 ORVNQPSIIGTATFYQYWSVRNRHRSRSGSVNTANHFNAWAOOGLTLGTMDOYI 180
Db 156 TRTNQPSIDGRTQFOQYWSVRQNRSSGVNMTKTFDAWASKMNLGSHYQIVATEGYF 215
Qy 181 SSGSASITVS 190
Db 216 SSGSASITVN 225

RESULT 12
Q8TG22 ID Q8TG22 PRELIMINARY; PRT; 225 AA.
AC Q8TG22;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Endo-1,4-xylanase.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu S., Sun J., Xu Z., Li W., Zhao H.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF490982; AAM08362.1; -
KW Xylan degradation; Hydrolase; Glycosidase.
SQ SEQUENCE 225 AA; 24127 MW; 5B14121662842A10 CRC64;

Query Match 63.7%; Score 665.5; DB 3; Length 225;
Best Local Similarity 65.6%; Pred. No. 1.4e-40;
Matches 120; Conservative 22; Mismatches 40; Indels 1; Gaps 1;
Qy 7 TGYNNGYFYSYWNDCGGVYTYNGPGQFSVNWNSGNFVGKGNPGTKNKNFNSGSY 66
Db 43 TGENNGFYFETDGGDVTYTNAGAGSYTVSWSNVGNFVGKGNPGSAQD-ITYSGTF 101
Qy 67 NPNGNSYLSVYGWSRNPLIEYIVENFGTYNPGTGTATKLGVEYTSFGSVYDIYRTQVNPQ 126
Db 102 TPGSNGYLSVYGWTDPLIEYIVESYDYNPGSGGTGTYKGTIVTSFGSVYDIYATRTNAA 161
Qy 127 SIIGTATFYQYWSVRNRHRSRSGSVNTANHFNAWAOOGLTLGTMDOYI 186
Db 162 SIQGTATFYQYWSVRQNRKRVCGTIVTSNHFNAWAKLGNLGNLTHNYQIVATEGYQSSGSS 221
Qy 187 ITV 189
Db 222 ITV 224

RESULT 13
Q9UUQ2 ID Q9UUQ2 PRELIMINARY; PRT; 221 AA.
AC Q9UUQ2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Xylanase A (EC 3.2.1.8).
GN XYNA.
OS Penicillium sp. 40.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX NCBI_TaxID=110511;

```

```

Db      41  TGTNGYYSFWTNGGGEVYTTNGDNGEYSVTWVDCDFTTSKGNWPNANA-QTVTVSGGEF 99
QY      67  NPNGNSYLSVYGWGRNPLIEYYIVENFGTYNPSTGATKLGCEVTSDSGVYDIYRTQRVNQP 126
Db      100  NPSGNAYLAVYGWTTDPLVEYYILESGYGNPSSGLTSLGQVTSDSGTYDIYSTQRVNQP 159
QY      127  SIIGTATFYQYWSVRNRHRRSSGVNTANHFNAWAQOGLTGLTMDYQIYVAVEGYFSSGSAS 186
Db      160  SIESTSTFNQYWSVRTEKRVGGTVTANHFNAWKALGLEMGTYNMINVSTEGYFSSGSST 219
QY      187  ITVS 190
Db      220  ITVS 223

RESULT 15
OL3447
ID      OL3447      PRELIMINARY;      PRT;      231 AA.
AC      OL3447;
DT      01-JAN-1998 (TREMBLrel. 05, Created)
DT      01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT      01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE      Beta-1,4-xylanase.
GN      XYL2
CO      Cochliobolus sativus (Bipolaris sorokiniana).
OC      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC      Pleosporales; Pleosporaceae; Cochliobolus.
ON      NCBI_TaxID=45130;
RX      [1]
RN      SEQUENCE FROM N.A.
RP      Emami K., Hack E.;
RT      "Characterization of a xylanase gene from Cochliobolus sativus and its
RT      expression.";
RL      Mycol. Res. 0:0-0(0).
DR      EMBL: AJ004802; CAA06151.1; -.
DR      HSSP: O43097; LYNA
DR      InterPro: IPR001137; GH_11.
DR      Pfam: PF00457; Glyco_hydro_11; 1.
DR      PRINTS; PR00911; GLHYDRASE11.
DR      PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR      PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW      Glycosidase; Hydrolase; Xylan degradation.
SQ      SEQUENCE 231 AA; 25577 MW; 333E6DD1F065A6BF CRC64;

Query Match 60.8%; Score 635.5; DB 3; Length 231;
Best Local Similarity 59.3%; Pred. No. 2.1e-38;
Matches 112; Conservative 26; Mismatches 50; Indels 1; Gaps 1
QY      1  OTIOPGTGYNHNGYFYSWNDHGCVTYTNGPGGQFSVNNKSNNGFVGGKGWQPGTKNKVI 60
Db      41  QSTPSSEGHNGYFYSWNTDGGSAQYTWGEGSRYSYTWRTNGFVGGKGNPGT-GRVI 99
QY      61  NFGSYNPNNGNSYLSVYGWGRNPLIEYYIVENFGTYNPSTGATKLGCEVTSDSGVYDIYRT 120
Db      100  NYGGAENPOGNGVLAVYGWTRNPLVEYYIESYGTYNPSSGAQVKGSGFOTDGGTYNVAVS 159
QY      121  QRVNQPSIIGTATFYQYWSVRNRHRRSSGVNTANHFNAWAQOGLTGLTMDYQIYVAVEGYF 180
Db      160  TRYQNPSIDGTRTFQOYWSVRQKRVGGSVNQNHFNAWSRYGLNIGOHYQIVATEGY 219
QY      181  SSGSASITV 189
Db      220  SSGSSDIYV 228

Search completed: May 9, 2003, 10:20:40
Job time : 32 secs

```

GenCore version 5.1.4_p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2003, 10:13:11 ; Search time 76 Seconds
(without alignments)
333.127 Million cell updates/sec

Title: US-09-990-874-16

Perfect score: 1045

Sequence: 1 QTIQPGTNGYNGYFYSYWND.....YQIVAVEGYFSGSASITVS 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```
A_Geneseq_101002.*
1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1045	100.0	190	19	Xylanase II of Tri
2	1045	100.0	190	21	T. reesei xylanase
3	1045	100.0	190	23	Trichoderma reesei
4	1045	100.0	223	14	pi 9.0 endoxylanase
5	1045	100.0	223	20	T. reesei xylanase
6	1042	99.7	190	23	Trichoderma reesei
7	1040	99.5	190	21	Trichoderma reesei
8	1038	99.3	190	19	Modified xylanase
9	1038	99.3	190	23	Trichoderma reesei
10	1035	99.0	190	19	Xylanase of Tricho

11	1035	99.0	190	21	AAV99681	T. viride xylanase
12	1035	99.0	190	23	AAE18453	Trichoderma viride
13	1030	98.6	190	21	AAV99735	Mutant T. reesei x
14	1029	98.5	190	23	AAE18495	Trichoderma reesei
15	1024	98.0	190	23	AAE18496	Trichoderma reesei
16	1023	97.9	190	23	AAE18472	Trichoderma reesei
17	1022	97.8	190	21	AAE18476	Trichoderma viride
18	1020	97.6	190	23	AAE18476	Trichoderma reesei
19	1017	97.3	190	23	AAE18474	Trichoderma reesei
20	1017	97.3	190	23	AAE18475	Trichoderma reesei
21	1017	97.3	190	23	AAE18482	Trichoderma reesei
22	1016	97.2	190	23	AAE18473	Trichoderma reesei
23	1016	97.2	223	19	AAW57422	Amino acid sequenc
24	1014	97.0	190	23	AAE18478	Trichoderma reesei
25	1014	97.0	190	23	AAE18481	Trichoderma reesei
26	1013	96.9	190	23	AAE18477	Trichoderma reesei
27	1013	96.9	190	23	AAE18480	Trichoderma reesei
28	1012	96.8	190	23	AAE18479	Trichoderma reesei
29	1010	96.7	190	23	AAE18483	Trichoderma reesei
30	1001	95.8	190	23	AAE18487	Trichoderma reesei
31	1000	95.7	190	23	AAE18484	Trichoderma reesei
32	1000	95.7	190	23	AAE18485	Trichoderma reesei
33	999	95.6	190	23	AAE18486	Trichoderma reesei
34	996	95.3	190	19	AAW60741	Xylanase of Tricho
35	996	95.3	190	21	AAV99678	T. harzianum xylan
36	996	95.3	190	23	AAE18450	Trichoderma reesei
37	994	95.1	190	23	AAE18458	Trichoderma reesei
38	993	95.0	190	23	AAE18489	Trichoderma reesei
39	992	94.9	190	19	AAW60282	Modified xylanase
40	990	94.7	190	21	AAE18453	Trichoderma harzia
41	990	94.7	190	21	AAV99736	Mutant T. reesei x
42	986	94.4	190	23	AAE18490	Trichoderma reesei
43	978	93.6	190	23	AAE18491	Trichoderma reesei
44	969	92.7	190	23	AAE18493	Trichoderma reesei
45	962	92.1	190	23	AAE18494	Trichoderma reesei

ALIGNMENTS

RESULT 1

AAW60743
ID AAW60743 standard; protein; 190 AA.
XX
AC AAW60743;
XX
XX
DT 02-SEP-1998 (first entry)
XX
DE Xylanase II of Trichoderma reesei.
XX
XX Family 11 xylanase; improve; thermophilicity; alkalophilicity;
KW thermotolerance; bleach; wood pulp; processing; wheat; maize;
KW digestibility-improving animal feed additive; starch production; mutant.
XX
OS Trichoderma reesei.

XX
XX EP828002-A2.

XX
XX 11-MAR-1998.

XX
XX 05-SEP-1997; 97EP-0115412.

XX
XX 09-SEP-1996; 96US-0709912.

XX
XX (CANADA) NAT RES COUNCIL CANADA.
XX (NARE-) NAT RES COUNCIL.

XX
XX Ishikawa K, Sung WL, Yaguchi M;

XX
XX WPI; 1998-161100/15.

XX
XX Modified xylanase enzymes - useful for improving wood pulp
PT bleaching, etc.

XX Disclosure; Page 48; 84pp; English.
 XX AAW60728-44 represent family 11 xylanases. The specification describes a
 CC method for modifying a family 11 xylanase to improve its
 CC thermophilicity, alkalophilicity and/or thermostability. This method
 CC comprises modification of amino acids 10, 27 or 29 of Trichoderma reesei
 CC xylanase II or corresponding aligned amino acid sequences in the
 CC xylanase, replacement of one or more amino acid sequences in the
 CC N-terminal region with corresponding aligned sequences from another
 CC family 11 xylanase to form a chimeric xylanase and/or upstream extension
 CC of the N terminus by addition of up to 10 amino acids. The modified
 CC xylanases are useful for improving the bleaching of wood pulp by
 CC treatment at 53-75 degrees celsius and pH 7.5-9.0 for 5-180 minutes. They
 CC might also be useful as digestibility-improving animal feed additives.
 CC They might also be useful in the processing of wheat or maize for starch
 CC production.
 XX Sequence 190 AA;
 SQ

Query Match 100.0%; Score 1045; DB 19; Length 190;
 Best Local Similarity 100.0%; Pred. No. 8.3e-90;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QTTPQGTGNGYFYSYWNDGCGVYTTNGPGGQFVSNNNSGNGFVGKQWPGTKNKVI 60
 Db 1 QTTPQGTGNGYFYSYWNDGCGVYTTNGPGGQFVSNNNSGNGFVGKQWPGTKNKVI 60
 QY 61 NFSGSYNPNNGNSVLSYVGSNRNPLIEYIVENFTYNPSTGATKLGVEVSDGSVYDIYRT 120
 Db 61 NFSGSYNPNNGNSVLSYVGSNRNPLIEYIVENFTYNPSTGATKLGVEVSDGSVYDIYRT 120
 QY 121 QRYNQPSIIIGTATFYQVWSVRRNRSSGSVNTANHFANAAQOGLTLGTMDYQIVAVEGYF 180
 Db 121 QRYNQPSIIIGTATFYQVWSVRRNRSSGSVNTANHFANAAQOGLTLGTMDYQIVAVEGYF 180
 QY 181 SSGSASITVS 190
 Db 181 SSGSASITVS 190

RESULT 2
 AAY99680
 ID AAY99680 standard; protein; 190 AA.
 AC AAY99680;
 XX
 DT 28-SEP-2000 (first entry)
 XX
 DE T. reesei xylanase, Xyn II.
 XX
 KW Xylanase; animal feed; digestion efficiency; thermostable;
 KW feed pelleting; enzyme; Xyn A; Xyn B; Xyn C; Xyn I; Xyn II.
 XX
 OS Trichoderma reesei.
 XX
 PN WO200029587-A1.
 XX
 XX 25-MAY-2000.
 XX
 PF 16-NOV-1999; 99WO-CA01093.
 XX
 PR 16-NOV-1998; 98US-0108504.
 XX
 PA (IOGE-) IOGEN CORP.
 XX
 XX Sung WL, Tolan JS;
 PI
 XX
 DR WPI: 2000-387799/33.
 DR N-PSDB: AAA48219.
 XX
 XX Thermostable xylanases useful for preparing animal feeds especially
 PT poultry or swine feed, exhibits optimal activity under physiological

PT conditions -
 XX Disclosure; Fig 1; 86pp; English.
 XX
 CC Xylanase enzymes are added to animal feeds to increase the efficiency of
 CC digestion and assimilation of nutrients. Xylanases are preferentially
 CC added during the feed pelleting process. To survive the pelleting
 CC process and to have optimum activity in the animal, the xylanase needs to
 CC have high thermostability, with optimum activity at physiological pH and
 CC temperature. The present sequence, xylanase Xyn II, from Trichoderma
 CC reesei, is a xylanase family 11 member. The xylanases of family
 CC 11 have several properties suitable for feed applications, however, they
 CC lack the thermostability required to survive food pelleting. The present
 CC sequence was used to identify non-conserved residues in family 11
 CC xylanases which could be mutated to introduce desirable properties e.g.
 CC thermostability. As a result various thermostable xylanases were
 CC identified (AAY99683, AAY99684, AAY99685, AAY99686, AAY99735 and
 CC AAY99736) which would be useful for animal feeds, especially poultry and
 CC swine feed.
 XX
 SQ Sequence 190 AA;

Query Match 100.0%; Score 1045; DB 21; Length 190;
 Best Local Similarity 100.0%; Pred. No. 8.3e-90;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QTTPQGTGNGYFYSYWNDGCGVYTTNGPGGQFVSNNNSGNGFVGKQWPGTKNKVI 60
 Db 1 QTTPQGTGNGYFYSYWNDGCGVYTTNGPGGQFVSNNNSGNGFVGKQWPGTKNKVI 60
 QY 61 NFSGSYNPNNGNSVLSYVGSNRNPLIEYIVENFTYNPSTGATKLGVEVSDGSVYDIYRT 120
 Db 61 NFSGSYNPNNGNSVLSYVGSNRNPLIEYIVENFTYNPSTGATKLGVEVSDGSVYDIYRT 120
 QY 121 QRYNQPSIIIGTATFYQVWSVRRNRSSGSVNTANHFANAAQOGLTLGTMDYQIVAVEGYF 180
 Db 121 QRYNQPSIIIGTATFYQVWSVRRNRSSGSVNTANHFANAAQOGLTLGTMDYQIVAVEGYF 180
 QY 181 SSGSASITVS 190
 Db 181 SSGSASITVS 190

RESULT 3
 AAE18452
 ID AAE18452 standard; Protein; 190 AA.
 XX
 AC AAE18452;
 XX
 DT 16-MAY-2002 (first entry)
 XX
 DE Trichoderma reesei xylanase (TRX), Xyn II.
 XX
 KW Modified xylanase; thermostability; alkalophilicity; industrial process;
 KW pulp manufacture; poultry; swine feed; enzyme; Xyn II.
 XX
 OS Trichoderma reesei.
 XX
 XX Key Location/Qualifiers
 FT Region 151..162
 FT /note="Helix"
 XX
 PN WO200192487-A2.
 XX
 XX 06-DEC-2001.
 PD
 PD 31-MAY-2001; 2001WO-CA00769.
 PF
 XX 31-MAY-2000; 2000US-213803P.
 PR
 XX (CANA) NAT RES COUNCIL CANADA.
 PA
 XX Sung WL;
 PI

XX WPI; 2002-171435/22.
 DR N-PSDB; AAD29410.
 XX
 PT Modified xylanase exhibiting increased thermostability and
 PT alkalophilicity useful for industrial processing e.g. for pulp
 PT manufacturing
 XX
 XX Disclosure: Page 80-81; 109pp; English.
 PS
 XX The present invention relates to a modified xylanase exhibiting increased
 CC thermostability and alkalophilicity. Modified xylanase is useful in
 CC industrial process such as pulp manufacturing. Modified xylanase is also
 CC useful for bleaching of pulp, processing of precision devices and
 CC improving digestibility of poultry and swine feed. Modified xylanase has
 CC improved performance at conditions of high temperature and pH and
 CC exhibits improved thermostability and/or alkalophilicity in comparison to
 CC corresponding native xylanase. The present sequence is
 CC Trichoderma reesei xylanase (TrX), Xyn II.
 XX
 SQ Sequence 190 AA;
 Query Match 100.0%; Score 1045; DB 23; Length 190;
 Best Local Similarity 100.0%; Pred. No. 8.3e-90;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 QTIQPGTGYNNGYFYSYWNDSGHTGVTYNGPGGFSVWNSGNGFVGGKQWPGCTKNKVI 60
 Db 1 QTIQPGTGYNNGYFYSYWNDSGHTGVTYNGPGGFSVWNSGNGFVGGKQWPGCTKNKVI 60
 Qy 61 NFSGSYNPNNGNSYLSVYGWSRNPLEYIYVENFGTYNPSTGATKLGEVTSQSVYDIYRT 120
 Db 61 NFSGSYNPNNGNSYLSVYGWSRNPLEYIYVENFGTYNPSTGATKLGEVTSQSVYDIYRT 120
 Qy 121 QRVNQPSTIGTATFYQYWSVRNRHRSRSGSVNTANHFNAWAQOGLTGTMDYQIIVAVEGYF 180
 Db 121 QRVNQPSTIGTATFYQYWSVRNRHRSRSGSVNTANHFNAWAQOGLTGTMDYQIIVAVEGYF 180
 Qy 131 SSGSASITVS 190
 Db 181 SSGSASITVS 190
 RESULT 4
 AAR47122
 ID AAR47122 standard; Protein; 223 AA.
 XX
 AC AAR47122;
 XX 10-JUN-1994 (first entry)
 XX
 XX pI 9.0 endoxylanase.
 DE
 DE Trichoderma reesei; enzyme; paper; pulp; food; feed industry;
 KW pI 5.5; pI 9.0; xln1; xln2; endoxylanase.
 XX
 XX Trichoderma reesei QM6a.
 XX
 FH Key Location/Qualifiers
 FT Protein 34..223
 FT /label= mat_protein
 FT Peptide 83..89
 FT /note= "sequence used for prepn. of PCR primer"
 FT Cleavage-site 19..20
 FT Modified-site 71
 FT /label= N-glycosylation_site
 FT Modified-site 94
 FT /label= N-glycosylation_site
 FT Active-site 119
 FT /note= "Glu proposed to be involved with an
 FT active site"
 FT Active-site 210
 FT /note= "Glu proposed to be involved with an

FT active site"
 XX WO9324621-A.
 PN
 XX
 PD 09-DEC-1993.
 XX
 PF 24-MAY-1993; 93WO-FI00221.
 XX
 XX 29-MAY-1992; 92US-0889893.
 XX
 XX (ALKO-) ALKO OY AB.
 XX
 XX Fagerstrom R, Lahtinen T, Nevalainen H, Paloheimo M;
 PI Saarelainen, Suominen P;
 XX
 XX WPI; 1993-405812/50.
 DR N-PSDB; AAQ54775.
 XX
 XX Isolated nucleic acid mol. used in enzymes for paper, pulp and
 PT feed industry - comprising sequence encoding aminoacid sequence
 PT of T. reesei pI 5.5 xylanase
 XX
 XX Claim 3; Page 77-78; 111pp; English.
 PS
 XX The T. reesei xln2 gene coding for the pI 9.0 endoxylanase was
 CC isolated from the wild-type strain QM6a. The gene contains one
 CC intron of 108 nucleotides and codes for a protein of 223 amino
 CC acids in which two putative N-glycosylation target sites were
 CC found. Three different T. reesei strains were transformed by
 CC targeting a construct composed of the xln2 gene with its own
 CC promoter to the endogenous cbh1 locus. Highest overall prodn.
 CC levels for xylanase were obtained using the T. reesei A.K02721,
 CC a genetically engineered strain, as a host. Integration into
 CC the cbh1 locus was not required for enhanced expression under
 CC xln2 promoter.
 XX
 SQ Sequence 223 AA;
 Query Match 100.0%; Score 1045; DB 14; Length 223;
 Best Local Similarity 100.0%; Pred. No. 1e-89;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 QTIQPGTGYNNGYFYSYWNDSGHTGVTYNGPGGFSVWNSGNGFVGGKQWPGCTKNKVI 60
 Db 34 QTIQPGTGYNNGYFYSYWNDSGHTGVTYNGPGGFSVWNSGNGFVGGKQWPGCTKNKVI 93
 Qy 61 NFSGSYNPNNGNSYLSVYGWSRNPLEYIYVENFGTYNPSTGATKLGEVTSQSVYDIYRT 120
 Db 94 NFSGSYNPNNGNSYLSVYGWSRNPLEYIYVENFGTYNPSTGATKLGEVTSQSVYDIYRT 153
 Qy 121 QRVNQPSTIGTATFYQYWSVRNRHRSRSGSVNTANHFNAWAQOGLTGTMDYQIIVAVEGYF 180
 Db 154 QRVNQPSTIGTATFYQYWSVRNRHRSRSGSVNTANHFNAWAQOGLTGTMDYQIIVAVEGYF 213
 Qy 181 SSGSASITVS 190
 Db 214 SSGSASITVS 223
 RESULT 5
 AAW67567
 ID AAW67567 standard; Protein; 223 AA.
 XX
 AC AAW67567;
 XX
 XX 02-MAR-1999 (first entry)
 DT
 XX T. reesei xylanase II protein.
 DE
 XX Xylanase; xln; reverse transcription; RT-PCR; primer; amplification;
 KW degradation; polymer; xylan; carbohydrate; plant; paper; pulp.
 XX
 OS Trichoderma reesei.

XX FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Peptide /note= "primary signal peptide"
 FT Peptide 20..33
 FT Protein /note= "propeptide"
 FT Protein 33..223
 FT Modified-site /note= "mature xylanase II protein"
 FT Modified-site 71
 FT Modified-site /note= "N-glycosylated"
 FT Modified-site 94
 FT Active-site /note= "N-glycosylated"
 FT Active-site 119
 FT Active-site /note= "active site residue"
 FT Active-site 210
 FT /note= "active site residue"
 PN US5837515-A.
 XX 17-NOV-1998.
 XX 16-SEP-1993; 93US-0121436.
 XX 16-SEP-1993; 93US-0121436.
 PR 16-MAY-1990; 90US-0524308.
 PR 29-MAY-1992; 92US-0889893.
 PR 24-MAY-1993; 93WO-FI00221.
 PR 18-JUN-1993; 93US-0078478.
 XX (ALKO-) ALKO-YHTIOET OY.
 XX Fagerstroem R, Nevalainen H, Paloheimo M, Saarelainen R;
 PI Suominen P;
 XX WPI: 1999-023453/02.
 DR N-PSDB; AAV81332.
 XX Nucleic acids encoding Trichoderma reesei xylanase(s) - useful for
 PT recombinant production of the enzyme, for use in paper and pulp
 PT production
 XX Claim 3; Fig 3A-B; 52pp; English.
 XX This sequence represents the Trichoderma reesei xylanase II enzyme
 CC (xln2) which has an isoelectric point (pI) of 9. The coding sequence
 CC was isolated by reverse transcription PCR using the primers
 CC AAV81333-V81335 based on amino acid sequence derived from the N-terminal
 CC of the purified protein. The encoded protein contains a 33 amino acid
 CC propeptide sequence with a primary signal peptide cleavage site between
 CC residues 19-20. The mature protein comprises 190 amino acids with a
 CC calculated molecular weight of 20.8 kD. The enzymes are used in the
 CC degradation of the polymer xylan, one of the most abundant carbohydrate
 CC components in plants. This is especially useful in the paper and pulp
 CC making industry.
 XX Sequence 223 AA;
 SQ
 Query Match 100.0%; Score 1045; DB 20; Length 223;
 Best Local Similarity 100.0%; Pred. No. 1e-89;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QTIQPTGYNNGYFFSYWNDHGHHGVTYTNPGGQSVNWSNNGNFVGGKGWPGTKNKVI 60
 DB 34 QTIQPTGYNNGYFFSYWNDHGHHGVTYTNPGGQSVNWSNNGNFVGGKGWPGTKNKVI 93
 QY 61 NFGSGYNPNNGNSVLSYVGWSRNPLIEYIYVENFGTYNPSTGATKLGCVTSDGSVDIYRT 120
 DB 94 NFGSGYNPNNGNSVLSYVGWSRNPLIEYIYVENFGTYNPSTGATKLGCVTSDGSVDIYRT 153
 QY 121 QRNVQPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAWAQQGLTLGTMDYQIVAVEGYF 180
 DB 154 QRNVQPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAWAQQGLTLGTMDYQIVAVEGYF 213

QY 181 SSGSASITVS 190
 DB 214 SSGSASITVS 223
 RESULT 6
 AAE18470
 ID AAE18470 standard; Protein; 190 AA.
 AC AAE18470;
 XX 16-MAY-2002 (first entry)
 DE Trichoderma reesei xylanase mutant, TrX-75A.
 KW Modified xylanase; thermostability; alkalophilicity; industrial process;
 XX pulp manufacture; poultry; swine feed; enzyme; mutant; muten.
 OS Trichoderma reesei.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT Misc-difference 75 /note= "Wild type Ser substituted with Ala"
 PN WO200192487-A2.
 PD 06-DEC-2001.
 XX 31-MAY-2001; 2001WO-CA00769.
 PR 31-MAY-2000; 2000US-213803P.
 XX (CANA) NAT RES COUNCIL CANADA.
 XX Sung WL;
 DR WPI: 2002-171435/22.
 PT Modified xylanase exhibiting increased thermostability and
 PT alkalophilicity useful for industrial processing e.g. for pulp
 PT manufacturing
 XX Claim 42; Page -: 109pp; English.
 XX The present invention relates to a modified xylanase exhibiting increased
 CC thermostability and alkalophilicity. Modified xylanase is useful in
 CC industrial process such as pulp manufacturing. Modified xylanase is also
 CC useful for bleaching of pulp, processing of precision devices and
 CC improving digestibility of poultry and swine feed. Modified xylanase has
 CC improved performance at conditions of high temperature and pH and
 CC exhibits improved thermostability and/or alkalophilicity in comparison to
 CC corresponding native xylanase. The present sequence is Trichoderma reesei
 CC xylanase (TrX) mutant.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from wild type xylanase referred as SEQ ID NO: 16 (AAE18452) and
 CC shown in page 80-81 of the specification.
 XX Sequence 190 AA;
 SQ
 Query Match 99.7%; Score 1042; DB 23; Length 190;
 Best Local Similarity 99.5%; Pred. No. 1.6e-89;
 Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QTIQPTGYNNGYFFSYWNDHGHHGVTYTNPGGQSVNWSNNGNFVGGKGWPGTKNKVI 60
 DB 1 QTIQPTGYNNGYFFSYWNDHGHHGVTYTNPGGQSVNWSNNGNFVGGKGWPGTKNKVI 60
 QY 61 NFGSGYNPNNGNSVLSYVGWSRNPLIEYIYVENFGTYNPSTGATKLGCVTSDGSVDIYRT 120
 DB 61 NFGSGYNPNNGNSVLSYVGWSRNPLIEYIYVENFGTYNPSTGATKLGCVTSDGSVDIYRT 120
 QY 121 QRNVQPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAWAQQGLTLGTMDYQIVAVEGYF 180

Db 121 QRYNPSIIIGTATFYQWSVRRNRSSGVSNTANHFNAWAQOGLTGLTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
Db 181 SSGSASITVS 190

RESULT 7
AAB48541
ID AAB48541 standard; Protein; 190 AA.

XX AC AAB48541;
XX DT 05-MAR-2001 (first entry)
XX DE Trichoderma reesei xyn II xylanase.
XX KW Bacterial; Bacillus circulans; xylanase; xylanase activity; XA;
XX KW bleaching agent.
XX OS Trichoderma reesei.
XX PN WO200068396-A2.
XX PD 16-NOV-2000.
XX PF 12-MAY-2000; 2000WO-US13172.
XX PR 12-MAY-1999; 99US-0133714.
XX PA (XENC-) XENCOR INC.
XX PI Bentzien JM;
XX DR WPI; 2000-679800/66.
XX Non naturally occurring XA protein with enhanced thermophilicity,
PT alkalophilicity or thermostability relative to the naturally occurring
PT Bacillus circulans xylanase is used in an agent for bleaching pulp -
XX Disclosure; Fig 16J; 114pp; English.

XX The present sequence is given in a specification relating to non
CC naturally occurring xylanase activity (XA) proteins. The XA proteins
CC comprise an amino acid sequence less than 97% identical to a naturally
CC occurring Bacillus circulans xylanase. They are modified to exhibit
CC enhanced thermophilicity, alkalophilicity or thermostability relative
CC to the naturally occurring B. circulans xylanase. They may be used as
CC the active compound in a bleaching agent which is used for bleaching
CC pulp.
XX Sequence 190 AA;

Query Match 99.5%; Score 1040; DB 21; Length 190;
Best Local Similarity 100.0%; Pred. No. 2.4e-89;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TIQPGTYNGYFYSYWNDCHGGVYTNPGGQFSVNSNSGPNFVGGKGWQPGTKNKVIN 61
Db 2 TIQPGTYNGYFYSYWNDCHGGVYTNPGGQFSVNSNSGPNFVGGKGWQPGTKNKVIN 61

QY 62 FSGSYNPNNGNSYLSVYGWSRNPILIEYIVENFCTYNPSTGATKLGVTSDGSVYDIYRTQ 121
Db 62 FSGSYNPNNGNSYLSVYGWSRNPILIEYIVENFCTYNPSTGATKLGVTSDGSVYDIYRTQ 121

QY 122 RVNQPSIIIGTATFYQWSVRRNRSSGVSNTANHFNAWAQOGLTGLTMDYQIVAVEGYFS 181
Db 122 RVNQPSIIIGTATFYQWSVRRNRSSGVSNTANHFNAWAQOGLTGLTMDYQIVAVEGYFS 181

QY 182 SSGSASITVS 190
Db 182 SSGSASITVS 190

RESULT 8
AAW60284

ID AAW60284 standard; protein; 190 AA.

XX AC AAW60284;

XX DT 02-SEP-1998 (first entry)

XX DE Modified xylanase II of Trichoderma reesei.

XX KW Family 11 xylanase; improve; thermophilicity; alkalophilicity;
XX KW thermotolerance; bleach; wood pulp; processing; wheat; maize;
XX KW digestibility-improving animal feed additive; starch production; mutant.

XX OS Synthetic.

XX OS Trichoderma reesei.

XX FH Key Location/Qualifiers

XX FT Misc-difference 14

XX FT /label= F14X

XX FT /note= "this residue can be Tyr or Phe"

XX PN EP828002-A2.

XX PD 11-MAR-1998.

XX PF 05-SEP-1997; 97EP-0115412.

XX PR 09-SEP-1996; 96US-0709912.

XX PA (CANADA) NAT RES COUNCIL CANADA.

XX PA (NARE-) NAT RES COUNCIL.

XX PI Ishikawa K, Sung WL, Yaguchi M;

XX WPI; 1998-161100/15.

XX Modified xylanase enzymes - useful for improving wood pulp
PT bleaching, etc.

PS Claim 5; Page -; 84pp; English.

XX The present sequence represents a modified xylanase of Trichoderma
CC reesei. The specification describes a method for modifying
CC a Family 11 xylanase to improve its thermophilicity, alkalophilicity
CC and/or thermotolerance. This method comprises modification of amino acids
CC 10, 14, 27 or 29 of Trichoderma reesei xylanase II or the corresponding
CC aligned amino acid sequences in the N-terminal region with corresponding
CC more amino acid sequences from another Family 11 xylanase to form a chimeric
CC xylanase and/or upstream extension of the N terminus by addition of upto
CC 10 amino acids. The modified xylanases are useful for improving the
CC bleachability of wood pulp by treatment at 55-75 degrees celsius and
CC pH 7.5-9.0 for 5-180 minutes. They might also be useful as
CC digestibility-improving animal feed additives. They might also be useful
CC in the processing of wheat or maize for starch production.
CC note: this sequence does not appear in the specification; it was created
CC using information provided.

XX Sequence 190 AA;

Query Match 99.3%; Score 1038; DB 19; Length 190;
Best Local Similarity 99.5%; Pred. No. 3.8e-89;
Matches 189; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QTQPGTYNGYFYSYWNDCHGGVYTNPGGQFSVNSNSGPNFVGGKGWQPGTKNKVI 60

Db 1 QTQPGTYNGYFYSYWNDCHGGVYTNPGGQFSVNSNSGPNFVGGKGWQPGTKNKVI 60

QY 61 NFSGSYNPNNGNSYLSVYGWSRNPILIEYIVENFCTYNPSTGATKLGVTSDGSVYDIYRT 120

Db 61 NFSGYNPNNGNSLSYVYWSNRNPLIEYYIVENFGTYNPSTGATKLGCVTSDGSVYDIYRT 120
QY 121 QRVNQPSIIIGTATFYQYWSVRNRHRRSSGVSNTANHFNAWAQOGLTLGTMDYQIIVAVEGYF 180
Db 121 QRVNQPSIIIGTATFYQYWSVRNRHRRSSGVSNTANHFNAWAQOGLTLGTMDYQIIVAVEGYF 180
QY 181 SSGSASITVS 190
Db 181 SSGSASITVS 190

RESULT 9
AAE18471
ID AAE18471 standard; Protein; 190 AA.
XX AC AAE18471;
DT 16-MAY-2002 (first entry)
XX DE Trichoderma reesei xylanase mutant, Trx-105H.
XX KW Modified xylanase; thermostability; alkalophilicity; industrial process;
KW pulp manufacture; poultry; swine feed; enzyme; mutant; mutain.
OS Trichoderma reesei.
OS Synthetic.
XX FH Key Location/Qualifiers
FT Misc-difference 105 /note= "Wild type Leu substituted with His"
XX PN WO200192487-A2.
XX PD 06-DEC-2001.
XX PF 31-MAY-2001; 2001WO-CA00769.
XX PR 31-MAY-2000; 2000US-213803P.
XX PA (CANA) NAT RES COUNCIL CANADA.
XX PI Sung WL;
XX WPI; 2002-171435/22.
XX Modified xylanase exhibiting increased thermostability and
PT alkalophilicity useful for industrial processing e.g. for pulp
PT manufacturing
XX Disclosure; Page -: 109pp; English.

XX The present invention relates to a modified xylanase exhibiting increased
CC thermostability and alkalophilicity. Modified xylanase is useful in
CC industrial process such as pulp manufacturing. Modified xylanase is also
CC useful for bleaching of pulp, processing of precision devices and
CC improving digestibility of poultry and swine feed. Modified xylanase has
CC improved performance at conditions of high temperature and pH and
CC exhibits improved thermostability and/or alkalophilicity in comparison to
CC corresponding native xylanase. The present sequence is Trichoderma reesei
CC xylanase (Trx) mutant.
CC Note: The present sequence is not shown in the specification but is
CC derived from wild type xylanase referred as SEQ ID NO: 16 (AAE18452) and
CC shown in page 80-81 of the specification.

XX Sequence 190 AA;
SQ

Query Match 99.3%; Score 1038; DB 23; Length 190;
Best Local Similarity 99.5%; Pred. No. 3.8e-89;
Matches 189; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QTIQPTGYNNGYFYSYWNDHGGVYTYTNGPGQFVSNNNSGNSFVGGKGPOTGNKVI 60
Db 1 QTIQPTGYNNGYFYSYWNDHGGVYTYTNGPGQFVSNNNSGNSFVGGKGPOTGNKVI 60

QY 61 NFSGYNPNNGNSLSYVYWSNRNPLIEYYIVENFGTYNPSTGATKLGCVTSDGSVYDIYRT 120
Db 61 NFSGYNPNNGNSLSYVYWSNRNPLIEYYIVENFGTYNPSTGATKLGCVTSDGSVYDIYRT 120
QY 121 QRVNQPSIIIGTATFYQYWSVRNRHRRSSGVSNTANHFNAWAQOGLTLGTMDYQIIVAVEGYF 180
Db 121 QRVNQPSIIIGTATFYQYWSVRNRHRRSSGVSNTANHFNAWAQOGLTLGTMDYQIIVAVEGYF 180
QY 181 SSGSASITVS 190
Db 181 SSGSASITVS 190

RESULT 10
AAW60744
ID AAW60744 standard; protein; 190 AA.
XX AC AAW60744;
DT 02-SEP-1998 (first entry)
XX DE Xylanase of Trichoderma viride.
XX KW Family 11 xylanase; improve; thermophilicity; alkalophilicity;
KW thermotolerance; bleach; wood pulp; processing; wheat; maize;
KW digestibility-improving animal feed additive; starch production; mutant.
XX OS Trichoderma viride.
XX PN EP828002-A2.
XX PD 11-MAR-1998.
XX PF 05-SEP-1997; 97EP-0115412.
XX PR 09-SEP-1996; 96US-0709912.
XX PA (CANA) NAT RES COUNCIL CANADA.
XX PA (NARE-) NAT RES COUNCIL.
XX PI Ishikawa K, Sung WL, Yaguchi M;
XX WPI; 1998-161100/15.
XX Modified xylanase enzymes - useful for improving wood pulp
PT bleaching, etc.
XX Disclosure; Pages 49-50; 84pp; English.

XX AAW60728-44 represent family 11 xylanases. The specification describes a
CC method for modifying a family 11 xylanase to improve its
CC thermophilicity, alkalophilicity and/or thermostolerance. This method
CC comprises modification of amino acids 10, 27 or 29 of Trichoderma reesei
CC xylanase II or corresponding aligned amino acids of another family 11
CC xylanase, replacement of one or more amino acid sequences in the
CC N-terminal region with corresponding aligned sequences from another
CC family 11 xylanase to form a chimeric xylanase and/or upstream extension
CC of the N terminus by addition of upto 10 amino acids. The modified
CC xylanases are useful for improving the bleachability of wood pulp by
CC treatment at 55-75 degrees celsius and pH 7.5-9.0 for 5-180 minutes. They
CC might also be useful as digestibility-improving animal feed additives.
CC They might also be useful in the processing of wheat or maize for starch
CC production.

XX Sequence 190 AA;
SQ

Query Match 99.0%; Score 1035; DB 19; Length 190;
Best Local Similarity 98.9%; Pred. No. 7.2e-89;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 QTIQPTGYNNGYFYSYWNDHGGVYTYTNGPGQFVSNNNSGNSFVGGKGPOTGNKVI 60
Db 1 QTIQPTGYNNGYFYSYWNDHGGVYTYTNGPGQFVSNNNSGNSFVGGKGPOTGNKVI 60

Db 1 QTIQPGTFNNGYFYSYWNDSHGCVTYTNGPGGQFSYVNSNSGNGFVGGKQWPGCTKNKVI 60
 QY 61 NFSGSYNPNNGNSYLSVYGWSRNPILIEYIIVENFGTYNPSTGATKLGVTSDGVSVDIYRT 120
 Db 61 NFSGSYNPNNGNSYLSVYGWSRNPILIEYIIVENFGTYNPSTGATKLGVTSDGVSVDIYRT 120
 QY 121 QRVNPSIICTATFYQYWSVRRNRHSSGVSNTANHFNAWAQOGLTLCMTDYQIIVAVEGYF 180
 Db 121 QRVNPSIICTATFYQYWSVRRNRHSSGVSNTANHFNAWAQOGLTLCMTDYQIIVAVEGYF 180
 QY 181 SSGSASITVS 190
 Db 181 SSGSASITVS 190

RESULT 11

AA99681
 ID AAY99681 standard; protein: 190 AA.

XX AC AAY99681;

XX DT 28-SEP-2000 (first entry)

XX DE T. viride xylanase, Xyn.

XX KW Xylanase; animal feed; digestion efficiency; thermostable;
 feed pelleting; enzyme; Xyn A; Xyn B; Xyn; Xyn C; Xyn I; Xyn II.

XX OS Trichoderma viride.

XX PN WO200029587-A1.

XX PD 25-MAY-2000.

XX PF 16-NOV-1999; 99WO-CA01093.

XX PR 16-NOV-1998; 98US-0108504.

XX PA (IÖGE-) IOGEN CORP.

XX PI Sung WL, Tolan JS;

XX DR WPI; 2000-387799/33.

XX PT Thermostable xylanases useful for preparing animal feeds especially
 poultry or swine feed, exhibits optimal activity under physiological
 conditions

XX PS Disclosure; Fig 1; 86pp; English.

XX CC Xylanase enzymes are added to animal feeds to increase the efficiency of
 digestion and assimilation of nutrients. Xylanases are preferentially
 added during the feed pelleting process. To survive the pelleting
 process and to have optimum activity in the animal, the xylanase needs to
 have high thermostability, with optimum activity at physiological pH and
 temperature. The present sequence, xylanase Xyn, from Trichoderma
 viride, is a xylanase Family 11 member. The xylanases of Family
 11 have several properties suitable for feed applications, however, they
 lack the thermostability required to survive food pelleting. The present
 sequence was used to identify non-conserved residues in Family 11
 xylanases which could be mutated to introduce desirable properties e.g.
 thermostability. As a result various thermostable xylanases were
 identified (AAY99683, AAY99684, AAY99685, AAY99686, AAY99735 and
 AAY99736) which would be useful for animal feeds, especially poultry and
 swine feed.

XX Sequence 190 AA;

Query Match 99.0%; Score 1035; DB 21; Length 190;

Best Local Similarity 98.9%; Pred. No. 7.2e-89;

Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QTIQPGTFNNGYFYSYWNDSHGCVTYTNGPGGQFSYVNSNSGNGFVGGKQWPGCTKNKVI 60

Db 1 QTIQPGTFNNGYFYSYWNDSHGCVTYTNGPGGQFSYVNSNSGNGFVGGKQWPGCTKNKVI 60
 QY 61 NFSGSYNPNNGNSYLSVYGWSRNPILIEYIIVENFGTYNPSTGATKLGVTSDGVSVDIYRT 120
 Db 61 NFSGSYNPNNGNSYLSVYGWSRNPILIEYIIVENFGTYNPSTGATKLGVTSDGVSVDIYRT 120
 QY 121 QRVNPSIICTATFYQYWSVRRNRHSSGVSNTANHFNAWAQOGLTLCMTDYQIIVAVEGYF 180
 Db 121 QRVNPSIICTATFYQYWSVRRNRHSSGVSNTANHFNAWAQOGLTLCMTDYQIIVAVEGYF 180
 QY 181 SSGSASITVS 190
 Db 181 SSGSASITVS 190

RESULT 12

AAE18453
 ID AAE18453 standard; Protein: 190 AA.

XX AC AAE18453;

XX DT 16-MAY-2002 (first entry)

XX DE Trichoderma viride xylanase, Xyn.

XX KW Modified xylanase; thermostability; alkalophilicity; industrial process;
 pulp manufacture; poultry; swine feed; enzyme; Xyn.

XX OS Trichoderma viride.

XX PN WO200192487-A2.

XX PD 06-DEC-2001.

XX PF 31-MAY-2001; 2001WO-CA00769.

XX PR 31-MAY-2000; 2000US-213803P.

XX PA (CANA) NAT RES COUNCIL CANADA.

XX PI Sung WL;

XX DR WPI; 2002-171435/22.

XX PT Modified xylanase exhibiting increased thermostability and
 alkalophilicity useful for industrial processing e.g. for pulp
 manufacturing

XX PS Disclosure; Page 81-82; 109pp; English.

XX CC The present invention relates to a modified xylanase exhibiting increased
 thermostability and alkalophilicity. Modified xylanase is useful in
 industrial process such as pulp manufacturing. Modified xylanase is also
 useful for bleaching of pulp, processing of precision devices and
 improving digestibility of poultry and swine feed. Modified xylanase has
 improved performance at conditions of high temperature and pH and
 exhibits improved thermostability and/or alkalophilicity in comparison to
 corresponding native xylanase. The present sequence is
 Trichoderma viride xylanase, Xyn.

XX Sequence 190 AA;

Query Match 99.0%; Score 1035; DB 23; Length 190;

Best Local Similarity 98.9%; Pred. No. 7.2e-89;

Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QTIQPGTFNNGYFYSYWNDSHGCVTYTNGPGGQFSYVNSNSGNGFVGGKQWPGCTKNKVI 60

Db 1 QTIQPGTFNNGYFYSYWNDSHGCVTYTNGPGGQFSYVNSNSGNGFVGGKQWPGCTKNKVI 60

QY 61 NFSGSYNPNNGNSYLSVYGWSRNPILIEYIIVENFGTYNPSTGATKLGVTSDGVSVDIYRT 120

Query Match 98.5%; Score 1029; DB 23; Length 190;
Best Local Similarity 98.4%; Pred. No. 2.6e-88;
Matches 187; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYWNDGHHGVTYTNPGGQFSVNNNSGNGFVGGKQWQPGTKNKVI 60
DB 1 QTIQPGTGYNNGYFYSYWNDGHHGVTYTNPGGQFSVNNNSGNGFVGGKQWQPGTKNKVI 60

QY 61 NFSGSYNPNNGSYLSVYGWSRNPLEYIYVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120
DB 61 NFSGSYNPNNGSYLSVYGWSRNPLEYIYVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120

QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTGLTMDYQIIVAVEGYF 180
DB 121 QRVNPSIIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAHGLHGLTMDYQIIVAVEGYF 180

QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 15
AAE18496
ID AAE18496 standard; Protein; 190 AA.
XX AAE18496;
AC
XX
DT 16-MAY-2002 (first entry)
XX
DE Trichoderma reesei xylanase mutant, Trx-157D-161R-162H-165H.
XX
KW Modified xylanase; thermostability; alkalophilicity; industrial process;
KW pulp manufacture; poultry; swine feed; enzyme; mutant; mutain.
XX
OS Trichoderma reesei.
OS Synthetic.

Key Location/Qualifiers
FT Misc-difference 157
FT /note= "Wild type Asn substituted with Asp"
FT Misc-difference 161
FT /note= "Wild type Gln substituted with Arg"
FT Misc-difference 162
FT /note= "Wild type Gln substituted with His"
FT Misc-difference 165
FT /note= "Wild type Thr substituted with His"

WO200192487-A2.
XX
XX
PD 06-DEC-2001.
XX
PF 31-MAY-2001; 2001WO-CA00769.
XX
PR 31-MAY-2000; 2000US-213803P.
XX
XX (CANA) NAT RES COUNCIL CANADA.
XX
XX Sung WL;
XX
XX WPI; 2002-171435/22.
XX
XX Modified xylanase exhibiting increased thermostability and
PT alkalophilicity useful for industrial processing e.g. for pulp
PT manufacturing -
XX
PS Claim 42; Page -; 109pp; English.
XX
XX The present invention relates to a modified xylanase exhibiting increased
CC thermostability and alkalophilicity. Modified xylanase is useful in
CC industrial process such as pulp manufacturing. Modified xylanase is also
CC useful for bleaching of pulp, processing of precision devices and
CC improving digestibility of poultry and swine feed. Modified xylanase has

CC improved performance at conditions of high temperature and pH and
CC exhibits improved thermophilicity and/or alkalophilicity in comparison to
CC corresponding native xylanase. The present sequence is Trichoderma reesei
CC xylanase (Trx) mutant.
CC Note: The present sequence is not shown in the specification but is
CC derived from wild type xylanase referred as SEQ ID NO: 16 (AAE18452) and
CC shown in page 80-81 of the specification.

XX
SQ Sequence 190 AA;

Query Match 98.0%; Score 1024; DB 23; Length 190;
Best Local Similarity 97.9%; Pred. No. 7.6e-88;
Matches 186; Conservative 2; Mismatches 2; Indels 3; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYWNDGHHGVTYTNPGGQFSVNNNSGNGFVGGKQWQPGTKNKVI 60
DB 1 QTIQPGTGYNNGYFYSYWNDGHHGVTYTNPGGQFSVNNNSGNGFVGGKQWQPGTKNKVI 60

QY 61 NFSGSYNPNNGSYLSVYGWSRNPLEYIYVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120
DB 61 NFSGSYNPNNGSYLSVYGWSRNPLEYIYVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120

QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAQOGLTGLTMDYQIIVAVEGYF 180
DB 121 QRVNPSIIIGTATFYQYWSVRNRHSSGVSNTANHFNAWAHGLHGLTMDYQIIVAVEGYF 180

QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

158 162 165

Search completed: May 9, 2003, 10:19:29
Job time : 77 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4_p5-4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2003, 10:14:01 ; Search time 24 Seconds
(without alignments)
328.354 Million cell updates/sec

Title: US-09-990-874-16

Perfect score: 1045

Sequence: 1 OTIQPGTGYNGYFYSYND.....YQIVAVEGYFSSGSATVS 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1045	100.0	222	1	XYN2	TRIIE	P36217 trichoderma
2	990	94.7	190	1	XYN	TRIHA	P48793 trichoderma
3	684.5	65.5	225	1	XYN1	EMENI	P55332 emeritella
4	676.5	64.7	225	1	XYNB	ASPAK	P48824 aspergillus
5	670.5	64.2	221	1	XYN2	EMENI	P55333 emeritella
6	664.5	63.6	225	1	XYN2	ASPNP	P55330 aspergillus
7	650.5	62.2	221	1	XYN1	COCCA	Q06562 cochliobolu
8	635.5	60.8	225	1	XYN1	THELA	O43097 thermomyces
9	614.5	58.8	227	1	XYN1	HUMIN	P55334 humicola in
10	594	56.8	335	1	XYNB	STRLI	P26515 streptomyce
11	575.5	55.1	644	1	XYNB	CELFI	P54865 cellulomona
12	571.5	54.7	233	1	XYN2	MAGGR	P55335 magnaporthe
13	565.5	54.1	197	1	XYN1	SCHCO	P35809 schizophyll
14	527	50.4	240	1	XYN1	STRLI	P26220 streptomyce
15	525.5	50.3	210	1	XYN1	BACST	P45705 bacillus st
16	503	48.1	213	1	XYN1	BACSU	P48429 bacillus su
17	502	48.0	213	1	XYN1	BACCI	P09850 bacillus ci
18	461	44.1	228	1	XYN1	BACPU	P00694 bacillus pu
19	453.5	43.4	261	1	XYN1	CLOSA	P17137 clostridium
20	444	42.5	512	1	XYN1	CLOSTR	P33558 clostridium
21	442.5	42.3	229	1	XYN1	TRIIE	P36218 trichoderma
22	430	41.1	211	1	XYN1	ASPNP	P55328 aspergillus
23	430	41.1	211	1	XYN1	ASPNP	P55329 aspergillus
24	428	41.0	211	1	XYN1	ASPTU	P55331 aspergillus
25	425	40.7	211	1	XYN3	ASPAK	P33557 aspergillus
26	402	38.5	954	1	XYN1	RUMFL	P29126 ruminococcu
27	383.5	36.7	802	1	XYNB	RUMFL	Q53317 ruminococcu
28	305	29.2	607	1	XYN1	NEOPA	P29127 neocalilmas
29	286.5	27.4	608	1	XYN1	FIBSU	P35811 fibrobacter
30	246	23.5	625	1	XYN1	PIRSP	Q12667 piromyces s
31	98.5	9.4	159	1	GRPA	MEDFA	Q09134 medicago fa
32	98	9.4	159	1	PHAL	PSELE	P2090 pseudomonas
33	95	9.1	1829	1	FRPC	NEIMB	Q91jv5 neisseria m

RESULT 1

ID	XYN2	TRIIE	STANDARD	PRT	222 AA
AC	P36217				
DT	01-JUN-1994	(Rel. 29, Created)			
DT	01-JUN-1994	(Rel. 29, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Endo-1,4-beta-xylanase 2 precursor (EC 3.2.1.8)	(Xylanase 2)			
DE	(1,4-beta-D-xylan xylanohydrolase 2)				
GN	XYN2				
OS	Trichoderma reesei (Hypocrea jecorina).				
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;				
OC	Hypocreales; Hypocreaceae; Hypocrea.				
OX	NCBI_TaxID=51453;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				
RC	STRAIN=C30;				
RX	MEDLINE=93103679; PubMed=1369024;				
RA	Toerrien A., Mach R.L., Messner R., Gonzalez R., Kalkkinen N.,				
RA	Harkki A., Kubicek C.P.;				
RT	"The two major xylanases from Trichoderma reesei: characterization of				
RT	both enzymes and genes."				
RL	Biotechnology 10:1461-1465(1992).				
RN	[2]				
RP	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).				
RC	STRAIN=C30;				
RX	MEDLINE=94283373; PubMed=8013449;				
RA	Toerrien A., Harkki A., Rouvinen J.;				
RT	"Three-dimensional structure of endo-1,4-beta-xylanase II from				
RT	Trichoderma reesei: two conformational states in the active site."				
RL	EMBO J. 13:2493-2501(1994).				
RN	[3]				
RP	X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).				
RC	STRAIN=C30;				
RX	MEDLINE=95127663; PubMed=7827044;				
RA	Toerrien A., Rouvinen J.;				
RT	"Structural comparison of two major endo-1,4-xylanases from				
RT	Trichoderma reesei."				
RL	Biochemistry 34:847-856(1995).				
RN	[4]				
RP	X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).				
RC	STRAIN=C30;				
RX	MEDLINE=96302263; PubMed=8755744;				
RA	Havukainen R., Toerrien A., Laitinen T., Rouvinen J.;				
RT	"Covalent binding of three epoxyalkyl xylosides to the active site of				
RT	endo-1,4-xylanase II from Trichoderma reesei."				
RL	Biochemistry 35:9617-9624(1996).				
CC	-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic				
CC	linkages in xylans.				
CC	-!- PATHWAY: Xylan degradation.				
CC	-!- PTH: THE N-TERMINUS IS BLOCKED.				
CC	-!- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL				
CC	HYDROLASES).				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation				

CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL: X69573; CAA49293.1; -
 DR PIR: S39154; S39154.
 DR PDB: 1XVO; 08-AUG-95.
 DR PDB: 1XVP; 08-AUG-95.
 DR PDB: 1ENX; 08-AUG-95.
 DR PDB: 1RED; 11-JAN-97.
 DR PDB: 1REE; 11-JAN-97.
 DR PDB: 1REF; 11-JAN-97.
 DR InterPro: IPR001137; GH_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Xylan degradation; Hydrolase; Glycosidase; Glycoprotein; Signal;
 KW 3D-structure.
 FT SIGNAL 1 32 ENDO-1,4-BETA-XYLANASE 2.
 FT CHAIN 33 222 NUCLEOPHILE.
 FT ACT_SITE 118 118 PROTON DONOR.
 FT ACT_SITE 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 222 AA; 24172 MW; 15F7032FACF963FF CRC64;

Query Match 100.0%; Score 1045; DB 1; Length 222;
 Best Local Similarity 100.0%; Pred. No. 2.8e-76;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTTPGTGYNNGYFYSYWNDGCGVYTNCGPGQFVSNVNSNGNFVGGKQWPGTKNKVI 60
 DB 33 QTTPGTGYNNGYFYSYWNDGCGVYTNCGPGQFVSNVNSNGNFVGGKQWPGTKNKVI 92
 QY 61 NFSGSYNPNGNSYLSVYGWSRNPLEYIYVENFGTYNPSTGATKLGVEVSDGSVDIYRT 120
 DB 93 NFSGSYNPNGNSYLSVYGWSRNPLEYIYVENFGTYNPSTGATKLGVEVSDGSVDIYRT 152
 QY 121 QRVNQPSSIIGTATFYQVWSVRRNHRSSGVSNTANHNANAAQGLTGTMDYQIVAVEGYF 180
 DB 153 QRVNQPSSIIGTATFYQVWSVRRNHRSSGVSNTANHNANAAQGLTGTMDYQIVAVEGYF 212
 QY 181 SSGSASITVS 190
 DB 213 SSGSASITVS 222

RESULT 2
 XYN_TRIHA STANDARD; PRT; 190 AA.
 AC P48793;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Endo-1,4-beta-xylanase (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylan
 DE xylanohydrolase).
 OS Trichoderma harzianum.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreales; mitosporic Hypocreales; Trichoderma.
 OX NCBI_TaxID=5544;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=E58;
 RA Yaguchi M., Roy C., Watson D.C., Rollin F., Tan L.U.L., Senior D.J.,
 RA Saddler J.N.
 RT "The amino acid sequence of the 20 kD xylanase from Trichoderma
 RT harzianum E58."
 RL (In) Visser J., Beldman G., Kusters-van Someren M.A.,
 RL Voragen A.G.J. (eds.);

RL Xylans and xylanases, pp.435-438, Elsevier, Amsterdam (1992).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
 RA Campbell R.L., Rose D.R., Wakarchuk W.W., To R.J., Sung W.,
 RA Yaguchi M.;
 RT "High-resolution structures of xylanases from B.circulans and
 RT T.harzianum identify a new folding pattern and implications for the
 RT atomic basis of the catalysis."
 RL (In) Suominen P., Reinikainen T. (eds.);
 RL Trichoderma reesei cellulases and other hydrolases, pp.63-72.
 RL Foundation for Biotechnical and Industrial Fermentation Research,
 RL Helsinki (1993).
 CC -|- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -|- PATHWAY: Xylan degradation.
 CC -|- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 DR PDB: 1XND; 20-DEC-94.
 DR InterPro: IPR001137; GH_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Xylan degradation; Hydrolase; Glycosidase; 3D-structure.
 FT ACT_SITE 86 86 NUCLEOPHILE.
 FT ACT_SITE 177 177 PROTON DONOR.
 FT SEQUENCE 190 AA; 20703 MW; 6A0F4D1C3599C698 CRC64;

Query Match 94.7%; Score 990; DB 1; Length 190;
 Best Local Similarity 94.2%; Pred. No. 5.5e-72;
 Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTTPGTGYNNGYFYSYWNDGCGVYTNCGPGQFVSNVNSNGNFVGGKQWPGTKNKVI 60
 DB 1 QTTPGTGYNNGYFYSYWNDGCGVYTNCGPGQFVSNVNSNGNFVGGKQWPGTKNKVI 60
 QY 61 NFSGSYNPNGNSYLSVYGWSRNPLEYIYVENFGTYNPSTGATKLGVEVSDGSVDIYRT 120
 DB 61 NFSGSYNPNGNSYLSVYGWSRNPLEYIYVENFGTYNPSTGATKLGVEVSDGSVDIYRT 120
 QY 121 QRVNQPSSIIGTATFYQVWSVRRNHRSSGVSNTANHNANAAQGLTGTMDYQIVAVEGYF 180
 DB 121 QRVNQPSSIIGTATFYQVWSVRRNHRSSGVSNTANHNANAAQGLTGTMDYQIVAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 3
 XYN1_EMENI STANDARD; PRT; 225 AA.
 AC P55332; Q00173;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Endo-1,4-beta-xylanase 1 precursor (EC 3.2.1.8) (Xylanase 1)
 DE (1,4-beta-D-xylan xylanohydrolase 1).
 OS Emericella nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=5072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96236210; PubMed=8787417;
 RA Perez-Gonzalez J.A., de Graaff L.H., Visser J., Ramon D.;
 RT "Molecular cloning and expression in Saccharomyces cerevisiae of two
 RT Aspergillus nidulans xylanase genes."
 RL Appl. Environ. Microbiol. 62:2179-2182(1996).
 CC -|- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -|- PATHWAY: Xylan degradation.
 CC -|- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL

CC EMBL; Z49893; CAA90074.1; 1.
DR HSSP; P48793; 1XND.
DR InterPro; IPR001137; GH_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 221 ENDO-1,4-BETA-XYLANASE 2.
FT ACT_SITE 117 117 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 208 208 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 221 AA; 23517 MW; 4266E580DDE9475 CRC64;

Query Match 64.2%; Score 670.5; DB 1; Length 221;
Best Local Similarity 65.8%; Pred. No. 1.5e-46;
Matches 121; Conservative 26; Mismatches 36; Indels 1; Gaps 1;

QY 7 TGYNNGYFYSYNDGHHGVTYTNPGQGFVSVMNSGNEFVGKQWPGTKNKVNFSGSY 66
DB 39 TGTSGGYYSFMTDGGDVTYTNPGQGFVSVMNSGNEFVGKQWPGTKNKVNFSGSY 97
QY 67 NPNGNSYLSVYGNSRNPLEYIVENFGYTNPSTGATKLGCEVTSVDSGVYDIYRTQVNOP 126
DB 98 IPGNGYLSVYGNGTNPLEYIVESYGDYNGTACHTGCTLESVDSGVYDIYRTATRENAP 157
QY 127 SIIGTATFYQYWSVRNRHSSGVSNTANFNHNAWAQOGLTGTMDYQIVAVEGYFSSGSAS 186
DB 158 SIIGTATFYQYWSVRNRHSSGVSNTANFNHNAWAQOGLTGTMDYQIVAVEGYFSSGSAS 217
QY 187 ITVS 190
DB 218 ITVS 221

RESULT 6
XYN2_ASPNG STANDARD; PRT; 225 AA.
AC P55330; Q12557;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE Endo-1,4-beta-xylanase II precursor (update)
DE Endo-1,4-beta-xylanase II precursor (EC 3.2.1.8) (Xylanase II)
DE (1,4-beta-D-xylan xylanohydrolase II).
GN XYNB.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO 4066;
RL Ito K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic linkages in xylans.
CC -!- PATHWAY: Xylan degradation.
CC -!- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL HYDROLASES).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).
CC EMBL; D38071; BAA07265.1;
DR HSSP; P09850; 1XNB.
DR InterPro; IPR001137; GH_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.

DR PRINTS; PR00911; GLHYDRASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 37 ENDO-1,4-BETA-XYLANASE II.
FT CHAIN 19 38 225 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 121 121 PROTON DONOR (BY SIMILARITY).
FT ACT_SITE 212 212 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 225 AA; 24057 MW; C4B8BB007AB2B8FD CRC64;

Query Match 63.6%; Score 664.5; DB 1; Length 225;
Best Local Similarity 65.6%; Pred. No. 4.4e-46;
Matches 120; Conservative 22; Mismatches 40; Indels 1; Gaps 1;

QY 7 TGYNNGYFYSYNDGHHGVTYTNPGQGFVSVMNSGNEFVGKQWPGTKNKVNFSGSY 66
DB 43 TGENNGYFYSFMTDGGDVTYTNPGQGFVSVMNSGNEFVGKQWPGTKNKVNFSGSY 101
QY 67 NPNGNSYLSVYGNSRNPLEYIVENFGYTNPSTGATKLGCEVTSVDSGVYDIYRTQVNOP 126
DB 102 TSGNGYLSVYGNGTNPLEYIVESYGDYNGTACHTGCTLESVDSGVYDIYRTATRNA 161
QY 127 SIIGTATFYQYWSVRNRHSSGVSNTANFNHNAWAQOGLTGTMDYQIVAVEGYFSSGSAS 186
DB 162 SIIGTATFYQYWSVRNRHSSGVSNTANFNHNAWAQOGLTGTMDYQIVAVEGYFSSGSAS 221
QY 187 ITV 189
DB 222 ITV 224

RESULT 7
XYN1_COCCA STANDARD; PRT; 221 AA.
AC Q06562;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase I precursor (EC 3.2.1.8) (Xylanase I)
DE (1,4-beta-D-xylan xylanohydrolase I).
GN XYL1.
OS Cochliobolus carbonum (Bipolaris zeicola).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Cochliobolus.
OX NCBI_TaxID=5017;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Race 1 / Isolate SB111;
RX MEDLINE=94003417; PubMed=8400376;
RA Apel P.C., Panaccione D.G., Holden F.R., Walton J.D.;
RT "Cloning and targeted gene disruption of xyl1, a beta 1,4-xylanase gene from the maize pathogen Cochliobolus carbonum";
RL Mol. Plant Microbe Interact. 6:467-473(1993).
RN [2]
RP PARTIAL SEQUENCE.
RA Holden F.R., Walton J.D.;
RT "Xylanases from the fungal maize pathogen Cochliobolus carbonum";
RL Physiol. Mol. Plant Pathol. 40:39-47(1992).
CC -!- FUNCTION: MAJOR XYLAN-DEGRADING ENZYME. CONTRIBUTES TO THE HYDROLYSIS OF ARABINOXYLAN, THE MAJOR COMPONENT OF MAIZE CELL-WALLS.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic linkages in xylans.
CC -!- PATHWAY: Xylan degradation.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: THE N-TERMINUS IS BLOCKED.
CC -!- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL HYDROLASES).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its


```
CC linkages in xylans.
CC -|- PATHWAY: Xylan degradation.
CC -|- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X76047; CAA53632.1; -
DR HSPB; 043097; LYNA.
DR InterPro; IPR001137; GH_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE1.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 19
FT CHAIN 20 227
FT ACT_SITE 121 121 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 212 212 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 227 AA; 25601 MW; 5C2FFGADCFEADALF CRC64;

Query Match 58.8%; Score 614.5; DB 1; Length 227;
Best Local Similarity 58.8%; Pred. No. 4.2e-42;
Matches 107; Conservative 26; Mismatches 48; Indels 1; Gaps 1;

QY 8 GYNGFYSYNDHGGVYITNGPGQFVSNMNSGNFVGGKQWPGTKNKVINFSGSYN 67
DB 44 GWHNGFYSWSDGGQVQYTNLEGSRYQVRWNTGNFVGGKGNPDT-GRITNYGGYFN 102
QY 68 PGNNSVLSYGVNSRNPLEYIVENGTYNPSTGATKLGVEVSDGSDYDIYRTORVQPS 127
DB 103 PQCGVLAVIGTRNPLVYVIESGTYNPGSQAYKGTFTYDQYDIFVSTRYNQPS 162
QY 128 IGTATFYQWYVRNRHRSRGSYNTANHNANAWAQOGLTGLTMDYQIVAVEGYFSSGASI 187
DB 163 IDGTRTFQYWSIRKKNKRVGSGVNMNHNANAWQHGMPLGQHYQYVAVVEGYOSSGESDI 222
QY 188 TV 189
DB 223 YV 224

RESULT 10
XYNB_STRLI STANDARD; PRT; 335 AA.
AC P26515;
DT 01-AUG-1992 (Rel. 23, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase B precursor (EC 3.2.1.8) (Xylanase B)
DE (1,4-beta-D-xylan xylanhidrolase B).
GN XLNB.
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1916;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 42-72.
RC STRAIN=66 / 1326;
RX MEDLINE=92077439; PubMed=1743521;
RA Shareck F., Roy C., Yaguchi M., Morosoli R., Kluepfel D.;
RT "Sequences of three genes specifying xylanases in Streptomyces
RL lividans."
RL Gene 107:75-82(1991).
RN [2]
RP REVISIONS TO 29-32 AND 252-307.
RC STRAIN=66 / 1326;
```

```
RX MEDLINE=95189090; PubMed=7533741;
RA Shareck F., Biely P., Morosoli R., Kluepfel D.;
RT "Analysis of DNA flanking the xlnB locus of Streptomyces lividans
RT reveals genes encoding acetyl xylan esterase and the RNA component of
RT ribonuclease P."
RL Gene 153:105-109(1995).
RN [3]
RP REVISION TO 225.
RA Shareck F.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: CONTRIBUTES TO HYDROLYSE HEMICELLULOSE. THE MAJOR
CC COMPONENT OF PLANT CELL-WALLS. XLNA AND XLNB SEEM TO ACT
CC SEQUENTIALLY ON THE SUBSTRATE TO YIELD XYLOBIOSIDE AND XYLOSE
CC AS CARBON SOURCES.
CC -|- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -|- PATHWAY: Xylan degradation.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M64552; AAC06114.2; -
DR HSPB; P09850; LXNB.
DR InterPro; IPR001137; GH_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE1.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 41
FT CHAIN 42 335
FT DOMAIN 42 230 ENDO-1,4-BETA-XYLANASE B.
FT DOMAIN 231 249 CATALYTIC.
FT DOMAIN 250 335 LINKER ("HINGE") (GLY-RICH BOX).
FT ACT_SITE 128 128 XYLAN-BINDING (POTENTIAL).
FT ACT_SITE 218 218 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 218 218 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 335 AA; 35575 MW; 513B1458BF8F0CF CRC64;

Query Match 56.8%; Score 594; DB 1; Length 335;
Best Local Similarity 55.1%; Pred. No. 2.7e-40;
Matches 109; Conservative 32; Mismatches 41; Indels 16; Gaps 5;

QY 5 PGT-----GYNNGYFYSYNDHGGVYITNGPGQFVSNMNSGNFVGGKQW 52
DB 36 PCTAQADTVTTTNOEGTNGNGYSEFTDSQGTVSMNMGGQYTSWRNTGNFVAGKGA 95
QY 53 PCTKNKVINFGSYNPNNGNLSYGVNSRNPLEYIVENGTYNPSTGATKLGVEVSDG 112
DB 96 NGCR-RTVQYSGSFNPSGNAYLALYXGWTSPNPLVEYIVDNWGTYP-R-TGEYK-GTVTSDG 152
QY 113 SYVDIYRTORVQPSIGTATGYQWYVRNRHRSRGSYNTANHNANAWAQOGLTGLTMD-Y 171
DB 153 GTYDIYKTRVKNKPSVEGTRTFDQYWSVRQSRKTGRTITTNHFNANAWARAGMPLGNFSY 212
QY 172 QIVAVEGYFSSGASITV 189
DB 213 MIMATEGYQSSGSSINV 230

RESULT 11
XYND_CELFI STANDARD; PRT; 644 AA.
AC P54865;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
```

15-JUN-2002 (Rel. 41, Last annotation update)
Endo-1,4-beta-xylanase D precursor (EC 3.2.1.8) (Xylanase D) (XYLD).
XND.
Cellulomonas fimi.
Bacteria; Actinobacteria; Actinobacteridae; Actinobacteridae;
Actinomycetales; Micrococciaceae; Cellulomonadaceae; Cellulomonas.
NCBI_TaxID=1708;
[1]
SEQUENCE FROM N.A.
STRAIN=221;
MEDLINE=94224155; PubMed=8170399;
RA Millward-Sadler S.J., Poole D.M., Henrissat B., Hazlewood G.P.,
Clarke J.H., Gilbert H.J.;
RT "Evidence for a general role for high-affinity non-catalytic
cellulose binding domains in microbial plant cell wall hydrolases."
RL Mol. Microbiol. 11:375-382(1994).
CC -1- FUNCTION: ENDOACTING XYLANASE WHICH DISPLAYS NO DETECTABLE
CC ACTIVITY AGAINST POLYSACCHARIDES OTHER THAN XYLAN. HYDROLYSES
CC GLUCOSIDIC BONDS WITH RETENTION OF ANOMERIC CONFIGURATION.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
CC or send an email to license@isb-sib.ch).

CC EMBL: X76729; CAA54145.1; .
CC HSP: P09850; L1XB.
CC InterPro: IPR001919; Bac_cellose-bind.
CC InterPro: IPR001137; GH_11.
CC Pfam: PF00457; Glyco_hydro_11; 1.
CC Pfam: PF00553; CBM_2; 2.
CC Pfam: PF01522; Polysac_deacet; 1.
CC PRINTS: PR00911; GLHYDRLASE1.
CC PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC Hydrolase: Glycosidase; Signal; Repeat.
CC SIGNAL 1 43 POTENTIAL.
CC CHAIN 44 644 ENDO-1,4-BETA-XYLANASE D.
CC DOMAIN 44 230 CATALYTIC
CC DOMAIN 231 245 LINKER ("HINGE") (GLY-RICH BOX).
CC DOMAIN 246 644 2 X 88 AA APPROXIMATE CBD-LIKE REPEATS.
CC REPEAT 246 333 1.
CC REPEAT 557 644 2.
CC DOMAIN 337 350 LINKER ("HINGE") (PRO-THR BOX).
CC DOMAIN 351 547 SOME, TO R. MELLITI NODB.
CC DOMAIN 548 556 LINKER ("HINGE") (GLY-RICH BOX).
CC DOMAIN 231 245 POLY-GLY.
CC DOMAIN 241 245 POLY-GLY.
CC DOMAIN 548 558 POLY-GLY.
CC DOMAIN 126 126 NUCLEOPHILE (BY SIMILARITY).
CC ACT_SITE 216 216 PROTON DONOR (BY SIMILARITY).
CC ACT_SITE 216 216 PROTON DONOR (BY SIMILARITY).
CC SEQUENCE 644 AA; 6581 MW; 56B045CC6E0E1820 CRC64;

Query Match 55.1%; Score 575.5; DB 1; Length 644;
Best Local Similarity 55.7%; Pred. No. 1.6e-38;
Matches 103; Conservative 39; Mismatches 38; Indels 5; Gaps 4;

QY 7 TGYNNGFYVSWNDHGGVYTYNGPGQFVSNVNSNGFVSGKQWPGCTKNKVI 66
DB 49 TGTGHDGYFSFWDTPSGVSNMDSNGSGYTRWNTGNTFVAGKGWSTGGR-KTVSYSCQF 106
QY 67 NPNGNSLVVYVWGRNPLIEYIVENFGTNPSTGATKGLGEVTSVSGVYDIYRTQRYNQ 126
DB 107 NPSRNYLTLLGWTQSPLEVIYIVDSNGTFRPT--GTFMGVTIVSDGGTYDIYRTQRYNKP 164

QY 127 SIITG-TATFYQYVSWNRHRSVNTANHFNAWAOOGLTGTMDYOIVAVEGYFSSGSA 185
DB 165 SIEGDSSTFYQYVSWNRQKRTGTTISGNHFDWASKGMNLGRHNYMIMATEGYSSGSS 224
QY 186 SITVS 190
DB 225 SITVS 229

RESULT 12
XYN2_MAGGR STANDARD; PRT; 233 AA.
ID XYN2_MAGGR
AC P55335; Q01171;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase 22 precursor (EC 3.2.1.8) (Xylanase 22)
DE (1,4-beta-D-xylan xylanohydrolase 22).
GN XYN22.
OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes; incertae sedis; Magnaportheaceae; Magnaporthe.
OX NCBI_TaxID=148305;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=KEN60-19;
RX MEDLINE=96172742; PubMed=8589407;
RA Wu S.C., Kaufman S., Darvill A.G., Albersheim P.;
RT "Purification, cloning and characterization of two xylanases from
RT Magnaporthe grisea, the rice blast fungus."
RL Mol. Plant Microbe Interact. 8:506-514(1995).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
CC or send an email to license@isb-sib.ch).

CC EMBL: L37529; AAC41683.1; .
CC HSP: O43097; LYNA.
CC InterPro: IPR001137; GH_11.
CC Pfam: PF00457; Glyco_hydro_11; 1.
CC PRINTS: PR00911; GLHYDRLASE1.
CC PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC Xylan degradation; Hydrolase; Glycosidase; Signal.
CC SIGNAL 1 39 POTENTIAL.
CC CHAIN 40 233 ENDO-1,4-BETA-XYLANASE 22.
CC ACT_SITE 126 126 NUCLEOPHILE (BY SIMILARITY).
CC ACT_SITE 217 217 PROTON DONOR (BY SIMILARITY).
CC SEQUENCE 233 AA; 25491 MW; 400963836F581F98 CRC64;

Query Match 54.7%; Score 571.5; DB 1; Length 233;
Best Local Similarity 51.8%; Pred. No. 1.1e-38;
Matches 99; Conservative 35; Mismatches 54; Indels 3; Gaps 2;

QY 1 OTIOPGTGYNNGFYVSWNDHGGVYTYNGPGQFVSNVNSNGFVSGKQWPGCTKNKVI 60
DB 40 QSTPSSTGRNGYIYVSWTDGASPVQYQNGSGYSYQWQSGGFGVGGKQWMPG-GSKSI 98
QY 61 NFGSSYNP--NGNSYLSVYVWGRNPLIEYIVENFGTNPSTGATKGLGEVTSVSGVYDIY 118
DB 99 TYSTCFPNVNGNAYLCIYQNTQNPVLEYILEYNGEYFNPCNSAQSRGTLCAGGTYTLH 158
QY 119 RTORVNOPSTIGTATFYQYVSWNRHRSVNTANHFNAWAOOGLTGTMDYOIVAVEG 178

```

Db 159 ESTRVNOPSIEGRTTFOQYWAIRQQRKNSGTVNTGFFQAWERAGRMGNHNYMIVATEG 218
QY 179 YFSSGSASITV 189
Db 219 YRSAGNSNINV 229

RESULT 13
XVNA_SCHCO STANDARD; PRT; 197 AA.
AC P35809;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase A (EC 3.2.1.8) (Xylanase A) (1,4-beta-D-xylan
DE xylanohydrolase A).
GN XVNA.
OS Schizophyllum commune (Bracket fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Schizophyllaceae; Schizophyllum.
OX NCBI_TaxID=5334;
RN [1]
RP SEQUENCE.
RC STRAIN-ATCC 38548 / Delmar;
RA Yaguchi M., Roy C., Ujite M., Watson D.C., Wakarchuk W.;
RL (in) Visser J., Beldman G., Kusters-van Sommeren M.A.,
RL Voragen A.G.J. (eds.);
RL Xylans and xylanases, pp.149-154, Elsevier, Amsterdam (1992).
RN [2]
RP SEQUENCE, AND DISULFIDE BONDS.
RC STRAIN-ATCC 38548 / Delmar;
RX MEDLINE=94063044; PubMed=8243636;
RA Oku T., Roy C., Watson D.C., Wakarchuk W., Campbell R., Yaguchi M.,
RA Jurasek L., Palce M.G.;
RT "Amino acid sequence and thermostability of xylanase A from
RT Schizophyllum commune.";
RT FEBS Lett. 334:296-300(1993).
RN [3]
RP PARTIAL SEQUENCE, AND ACTIVE SITE GLU-87.
RC STRAIN-ATCC 38548 / Delmar;
RX MEDLINE=94155888; PubMed=7906649;
RA Bray M.R., Clarke A.J.;
RT "Identification of a glutamate residue at the active site of xylanase
RT A from Schizophyllum commune.";
RL Eur. J. Biochem. 219:821-827(1994).
CC -|- FUNCTION: HYDROLYSES XYLANS INTO XYLOBIOSIDE AND XYLOSE. THIS
CC XYLANASE HAS A VERY BROAD PH ACTIVITY.
CC -|- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -|- PATHWAY: Xylan degradation.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
DR PIR: S38973; S38973.
DR PIR: A44597; A44597.
DR HSP: Q43097; IYNA.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro.11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation; Hydrolase; Glycosidase.
FT ACT_SITE 87 87 NUCLEOPHILE (PROBABLE).
FT ACT_SITE 184 184 PROTON DONOR (BY SIMILARITY).
FT DISULFID 111 160
SQ SEQUENCE 197 AA; 20978 MW; 42C8074E67C1FBE9 CRC64;

Query Match 54.1%; Score 565.5; DB 1; Length 197;
Best Local Similarity 55.0%; Pred. No. 2.8e-38;
Matches 105; Conservative 34; Mismatches 45; Indels 7; Gaps 3;
QY 7 TGYNGYFFSYNDGGHYTYTNGQGFVNVNS-NSGNFVGKGWQPCTKKNVNFSGS.65

```

```

Db 7 TCTDGGYYTSMWTDGAGDATYQNGGGSYTLTWSGNGNLVGGKWNPGAAASRISYSGT 66
QY 66 YNPNGNSYLSVYGSWRNPLIEYIVENFTYNPSTGATKLGVTSDGSYVDIYRTORVNO 125
Db 67 YQPNGNSYLSVYGVWTRSSLIIEYIVESYSDPSSAASHKSGVTCNGATYDILSTRVNA 126
QY 126 PSIIATPATTYQVWSVRRNHR-----SGSVNTANHFNAWAQQGLTLGT-MDYQIVAVEGY 179
Db 127 PSIDGTQTFEQFWSVRNPKKAPGSGISGTVQCHDFDANKGLGMNLGSEHNTQIVATEGY 186
QY 180 FSSGSASITVS 190
Db 187 QSSGTATITVT 197

RESULT 14
XVNC_STRLI STANDARD; PRT; 240 AA.
AC P26220;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase C precursor (EC 3.2.1.8) (Xylanase C)
DE (1,4-beta-D-xylan xylanohydrolase C).
GN XLNC.
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1916;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 50-80.
RC STRAIN=66 / 1326;
RX MEDLINE=92077439; PubMed=1743521;
RA Shareck F., Roy C., Yaguchi M., Morosoli R., Kluepfel D.;
RT "Sequences of three genes specifying xylanases in Streptomyces
RT lividans.";
RL Gene 107:75-82(1991).
CC -|- FUNCTION: CONTRIBUTES TO HYDROLYSE HEMICELLULOSE, THE MAJOR
CC COMPONENT OF PLANT CELL-WALLS.
CC -|- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -|- PATHWAY: Xylan degradation.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
DR EMBL: M64553; AAA26836.1; -.
DR EMBL: A25307; CAA01768.1; -.
DR PIR: JS0591; JS0591.
DR HSP: P09850; IXNB.
DR InterPro: IPR001137; GH_11.
DR Pfam: PF00457; Glyco_hydro.11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 49
FT CHAIN 50 240 ENDO-1,4-BETA-XYLANASE C.
FT ACT_SITE 134 134 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 226 226 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 240 AA; 25673 MW; FC663415780142CA CRC64;

Query Match 50.4%; Score 527; DB 1; Length 240;
Best Local Similarity 53.1%; Pred. No. 3.9e-35;

```

[illegible]

RESULT 15
XYNA_BACST
ID XYNA_BACST
STANDARD: PRT: 210 AA.

```

RESULT 15
XYNA_BACST
ID XYNA_BACST STANDARD; PRT; 210 AA.
AC P45705;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 13-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A)
DE (1,4-beta-D-xylan xylanhydrolase A).
GN XYNA.
OS Bacillus steartothermophilus.
OC Bacteria; Firmicutes; Bacillales; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=NO. 236;
RA Cho S., Choi Y.;
RT "Nucleotide sequence analysis of an endo-xylanase gene (xyna) from
RT Bacillus steartothermophilus."
RL J. Microbiol. Biotechnol. 5:117-124(1995).
RN [2]
RN REVISIONS.
RC STRAIN=NO. 236;
RA Cho S., Choi Y.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC of the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U15985; AAB72117.1;
CC DR HSSP: P09850; LXNB
CC DR InterPro: IPR001137; GH_11.
CC DR Pfam: PF00457; Glyco_hydro_11; 1.
CC DR PRINTS; PR00911; GLHYDLASE1.
CC DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC DR PROSITE; PS00777; GLYCOSYL_HYDROL_F12_1; 1.
CC KW Xylan degradation; Hydrolase; Glycosidase; Signal.
CC FT SIGNAL 1
CC FT CHAIN 19 POTENTIAL.
CC FT ACT_SITE 20 210 ENDO-1,4-BETA-XYLANASE A.
CC FT ACT_SITE 104 104 NUCLEOPHILE (BY SIMILARITY).
CC FT ACT_SITE 197 197 PROTON DONOR (BY SIMILARITY).
CC SQ SEQUENCE 210 AA; 23221 MW; 3190CF74C34AAB45 CRC64;
Query Match 50.3%; Score 525.5; DB 1; Length 210;

```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4_p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2003, 10:01:05 ; Search time 30 Seconds
(without alignments)
186.345 Million cell updates/sec

Title: US-09-990-874-16

Perfect score: 1045

Sequence: 1 QTIQPGTGYNGYFYWYND.....YQIVAVEGYFSGSASITVS 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1045	100.0	190	1	US-08-044-621D-26
2	1045	100.0	190	1	US-08-709-912-16
3	1045	100.0	190	2	US-09-047-370-16
4	1045	100.0	223	2	US-08-121-436A-2
5	1035	99.0	190	1	US-08-709-912-17
6	1035	99.0	190	2	US-09-047-370-17
7	1032	98.8	190	1	US-08-044-621D-27
8	1016	97.2	223	4	US-09-254-733-7
9	996	95.3	190	1	US-08-044-621D-28
10	996	95.3	190	1	US-08-709-912-14
11	996	95.3	190	2	US-09-047-370-14
12	721.5	69.0	261	4	US-08-768-373-2
13	665.5	63.7	225	1	US-08-290-979A-8
14	656.5	62.8	230	4	US-08-768-373-4
15	635.5	60.8	225	2	US-08-886-765-2
16	635.5	60.8	225	4	US-09-115-660-2
17	630	60.3	231	2	US-08-902-655A-6
18	630	60.3	296	3	US-08-507-431-6
19	630	60.3	296	3	US-09-116-622-6
20	630	60.3	296	4	US-09-219-277-6
21	630	60.3	296	4	US-09-599-661-6
22	620.5	59.4	227	1	US-08-458-023B-4
23	607.5	58.1	189	1	US-08-709-912-13
24	607.5	58.1	189	2	US-09-047-370-13
25	595.5	57.0	344	2	US-08-468-812-2
26	595.5	57.0	344	4	US-08-590-563-2
27	591	56.6	206	1	US-08-315-695-19

Sequence 34, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 29, Appl
Sequence 9, Appl
Sequence 2, Appl
Sequence 1, Appl
Sequence 33, Appl
Sequence 13, Appl
Sequence 12, Appl
Sequence 35, Appl
Sequence 20, Appl
Sequence 2, Appl
Sequence 11, Appl
Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-08-044-621D-26

; Sequence 26, Application US/08044621D

; Patent No. 5405769

; GENERAL INFORMATION:

; APPLICANT: Warren W. Wakarchuk

; APPLICANT: Wing L. Sung

; APPLICANT: Makoto Yaguchi

; APPLICANT: Robert L. Campbell

; APPLICANT: David R. Rose

; TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS

; TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Gowling, Strathy & Henderson

; STREET: Suite 2600, 160 Elgin Street

; CITY: Ottawa

; STATE: Ontario

; COUNTRY: Canada

; ZIP: K1P 1C3

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 in., 360kB storage

; COMPUTER: IBM PC

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/044,621D

; FILING DATE: April 8, 1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Judy A. Erratt

; REGISTRATION NUMBER: 34,076

; REFERENCE/DOCKET NUMBER: 08-863796

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 613-786-0199

; TELEFAX: 613-563-9869

; TELEX:

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 190

; TYPE: Amino Acid

; STRANDEDNESS: No. 5405769 Relevant

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; DESCRIPTION: NO

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

```

; FRAGMENT TYPE: NO
; ORIGINAL SOURCE:
; ORGANISM: Trichoderma reesei
; STRAIN: Trichoderma reesei, XYN II, 21kD, pi 9.0
; IMMEDIATE SOURCE:
; POSITION IN GENOME:
; FEATURE:
; PUBLICATION INFORMATION:
; AUTHORS: Torionene, A., Mach, R.L., Messner, R.,
; AUTHORS: Gonzalez, R., Kalkkinen, N., Harkki, A.
; AUTHORS: & Kubicek, C.P.
; TITLE:
; JOURNAL: Bio/Technology
; VOLUME: 10
; ISSUE:
; PAGES: 1461-1465
; DATE: 1992
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-26

Query Match 100.0%; Score 1045; DB 1; Length 190;
Best Local Similarity 100.0%; Pred. No. 5e-90;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTTPGTGYNNGYFFSYWNDGHHGVTYTNPGGQFSVNNNSGNGFVGGKQWPGTKNKVI 60
DB 1 QTTPGTGYNNGYFFSYWNDGHHGVTYTNPGGQFSVNNNSGNGFVGGKQWPGTKNKVI 60

QY 61 NFSGSYNPNNGNSVLSVYGWSRNPLEYIYVENFGTNPSTGATKLGCVTSDGSVDIYRT 120
DB 61 NFSGSYNPNNGNSVLSVYGWSRNPLEYIYVENFGTNPSTGATKLGCVTSDGSVDIYRT 120

QY 121 QRYNQPSSIIGTATFYQYWSVRRNRHSSGVSNTANHFNAWAQQGLTGLTMDYQIVAVEGYF 180
DB 121 QRYNQPSSIIGTATFYQYWSVRRNRHSSGVSNTANHFNAWAQQGLTGLTMDYQIVAVEGYF 180

QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 2
US-08-709-912-16
; Sequence 16, Application US/08709912
; Patent No. 5759840
; GENERAL INFORMATION:
; APPLICANT: Sung Dr., Wing L
; APPLICANT: Yaguchi Dr., Makoto
; APPLICANT: Ishikawa Dr., Kazuhiko
; TITLE OF INVENTION: Modification of Xylanase to Improve
; TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
; TITLE OF INVENTION: Thermostability
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
; STREET: 277 Park Ave.
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10172-0194
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,912
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Olsen Mr, Warren E
; REGISTRATION NUMBER: 27290
; REFERENCE/DOCKET NUMBER: 1039.2000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-2400
; TELEFAX: (212) 758-2982
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 190 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Internal
; ORIGINAL SOURCE:
; ORGANISM: Trichoderma reesei
; STRAIN: xyn II
; PUBLICATION INFORMATION:
; AUTHORS: Torionene, A
; AUTHORS: Mach, R. L.
; AUTHORS: Messner, R.
; AUTHORS: Gonzalez, R.
; AUTHORS: Kalkkinen, N
; AUTHORS: Harkki, A
; AUTHORS: Kubicek, C. P.
; JOURNAL: Biotechnology
; VOLUME: 10
; PAGES: 1461-1465
; DATE: 1992
; US-08-709-912-16

Query Match 100.0%; Score 1045; DB 1; Length 190;
Best Local Similarity 100.0%; Pred. No. 5e-90;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTTPGTGYNNGYFFSYWNDGHHGVTYTNPGGQFSVNNNSGNGFVGGKQWPGTKNKVI 60
DB 1 QTTPGTGYNNGYFFSYWNDGHHGVTYTNPGGQFSVNNNSGNGFVGGKQWPGTKNKVI 60

QY 61 NFSGSYNPNNGNSVLSVYGWSRNPLEYIYVENFGTNPSTGATKLGCVTSDGSVDIYRT 120
DB 61 NFSGSYNPNNGNSVLSVYGWSRNPLEYIYVENFGTNPSTGATKLGCVTSDGSVDIYRT 120

QY 121 QRYNQPSSIIGTATFYQYWSVRRNRHSSGVSNTANHFNAWAQQGLTGLTMDYQIVAVEGYF 180
DB 121 QRYNQPSSIIGTATFYQYWSVRRNRHSSGVSNTANHFNAWAQQGLTGLTMDYQIVAVEGYF 180

QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 3
US-09-047-370-16
; Sequence 16, Application US/09047370
; Patent No. 5866408
; GENERAL INFORMATION:
; APPLICANT: Sung Dr., Wing L
; APPLICANT: Yaguchi Dr., Makoto
; APPLICANT: Ishikawa Dr., Kazuhiko
; TITLE OF INVENTION: Modification of Xylanase to Improve
; TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
; TITLE OF INVENTION: Thermostability
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
; STREET: 277 Park Ave.
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10172-0194

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039,2000
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma reesei
STRAIN: Xyn II
PUBLICATION INFORMATION:
AUTHORS: Torronene, A
AUTHORS: Mach, R. L.
AUTHORS: Messner, R
AUTHORS: Gonzalez, R
AUTHORS: Kalkinen, N
AUTHORS: Harkki, A
AUTHORS: Kubicek, C. P.
JOURNAL: Biotechnology
VOLUME: 10
PAGES: 1461-1465
DATE: 1992
US-09-047-370-16

Query Match 100.0%; Score 1045; DB 2; Length 190;
Best Local Similarity 100.0%; Pred. No. 5e-90;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OTTQPGTYNGYFYSYWNDGCHGVYTYNGPGQFVSYNWNSGNFVGKQWPGTKNKVI 60
Db 1 OTTQPGTYNGYFYSYWNDGCHGVYTYNGPGQFVSYNWNSGNFVGKQWPGTKNKVI 60
QY 61 NFGSGYNPNCGNSVLSVYGWNRNPLIEYIYVENFGTYNPSTGATKLGCVTSDGVSVDIYRT 120
Db 61 NFGSGYNPNCGNSVLSVYGWNRNPLIEYIYVENFGTYNPSTGATKLGCVTSDGVSVDIYRT 120
QY 121 QRVNQPSSIIGTATFYQYWSVRRNRHSSGSVNTANHFNAWAQOGLTLGTMDYQIVAVEGYF 180
Db 121 QRVNQPSSIIGTATFYQYWSVRRNRHSSGSVNTANHFNAWAQOGLTLGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
Db 181 SSGSASITVS 190

RESULT 4

US-08-121-436A-2
Sequence 2, Application US/08121436A
Patent No. 5837515
GENERAL INFORMATION:
APPLICANT: Suominen, Pirkko

APPLICANT: Nevalainen, Helena
APPLICANT: Saarelainen, Ritva
APPLICANT: Paloheimo, Marja
APPLICANT: Lahtinen, Tarja
APPLICANT: Fagerstr m, Richard
TITLE OF INVENTION: No. 5837515el Enzyme Preparations and Methods
TITLE OF INVENTION: for Their Production
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,436A
FILING DATE: 16-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,478
FILING DATE: 18-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FI93/00221
FILING DATE: 24-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,893
FILING DATE: 29-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/524,308
FILING DATE: 16-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Cimbalala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.008000C
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-121-436A-2

Query Match 100.0%; Score 1045; DB 2; Length 223;
Best Local Similarity 100.0%; Pred. No. 6.1e-90;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OTTQPGTYNGYFYSYWNDGCHGVYTYNGPGQFVSYNWNSGNFVGKQWPGTKNKVI 60
Db 34 OTTQPGTYNGYFYSYWNDGCHGVYTYNGPGQFVSYNWNSGNFVGKQWPGTKNKVI 93
QY 61 NFGSGYNPNCGNSVLSVYGWNRNPLIEYIYVENFGTYNPSTGATKLGCVTSDGVSVDIYRT 120
Db 94 NFGSGYNPNCGNSVLSVYGWNRNPLIEYIYVENFGTYNPSTGATKLGCVTSDGVSVDIYRT 153
QY 121 QRVNQPSSIIGTATFYQYWSVRRNRHSSGSVNTANHFNAWAQOGLTLGTMDYQIVAVEGYF 180
Db 154 QRVNQPSSIIGTATFYQYWSVRRNRHSSGSVNTANHFNAWAQOGLTLGTMDYQIVAVEGYF 213
QY 181 SSGSASITVS 190
Db 214 SSGSASITVS 223

RESULT 5

US-08-709-912-17

Sequence 17, Application US/08709912
Patent No. 5759840
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of xylanase to improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma viride
PUBLICATION INFORMATION:
AUTHORS: Yaguchi, M
AUTHORS: Roy, C
AUTHORS: Ujile, M
AUTHORS: Watson, D. C.
AUTHORS: Wakarchuk, W.
JOURNAL: Xylan and Xylanase
PAGES: 149-154
DATE: 1992
US-08-709-912-17

Query Match 99.0%; Score 1035; DB 1; Length 190;
Best Local Similarity 98.9%; Pred. No. 4.3e-89;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 QTIPQCTGYNNGYFFSYWNDHGGVYTTNGPGQFSVNMNSGNGFVGGKQWPGTKNKVI 60
DB 1 QTIPQCTGYNNGYFFSYWNDHGGVYTTNGPGQFSVNMNSGNGFVGGKQWPGTKNKVI 60
QY 61 NFGSGYNPNNGSVLSYVGNRPDIYYIVENFGTYNPSTGATKLGVTSDGSVDIYRT 120
DB 61 NFGSGYNPNNGSVLSYVGNRPDIYYIVENFGTYNPSTGATKLGVTSDGSVDIYRT 120
QY 121 QRYNQPSIIIGTATFYQYWSVRRNRSSGSVNTANHFNAWAQQGLTLGTMDYQIVAVEGYF 180
DB 121 QRYNQPSIIIGTATFYQYWSVRRNRSSGSVNTANHFNAWAQQGLTLGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190

DB 181 SSGSASITVS 190
RESULT 6
US-09-047-370-17
Sequence 17, Application US/09047370
Patent No. 5866408
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of xylanase to improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 09-SEP-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma viride
PUBLICATION INFORMATION:
AUTHORS: Yaguchi, M
AUTHORS: Roy, C
AUTHORS: Ujile, M
AUTHORS: Watson, D. C.
AUTHORS: Wakarchuk, W.
JOURNAL: Xylan and Xylanase
PAGES: 149-154
DATE: 1992
US-09-047-370-17

Query Match 99.0%; Score 1035; DB 2; Length 190;
Best Local Similarity 98.9%; Pred. No. 4.3e-89;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 QTIPQCTGYNNGYFFSYWNDHGGVYTTNGPGQFSVNMNSGNGFVGGKQWPGTKNKVI 60
DB 1 QTIPQCTGYNNGYFFSYWNDHGGVYTTNGPGQFSVNMNSGNGFVGGKQWPGTKNKVI 60

Qy 61 NFSGSYNPNNGSYLSVYGSWRNPLIEYIVENFGTYNPNSTGATKLGVTSDGSVYDIYRT 120
 Db 61 NFSGSYNPNNGSYLSVYGSWRNPLIEYIVENFGTYNPNSTGATKLGVTSDGSVYDIYRT 120
 Qy 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAWAQOGLTGLTMDYQIVAVEGYF 180
 Db 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAWAQOGLTGLTMDYQIVAVEGYF 180
 Qy 181 SSGSASITVS 190
 Db 181 SSGSASITVS 190

RESULT 7
 US-08-044-621D-27
 ; Sequence 27, Application US/08044621D
 ; Patent No. 5405769
 ; GENERAL INFORMATION:
 ; APPLICANT: Warren W. Wakarchuk
 ; APPLICANT: Wing L. Sung
 ; APPLICANT: Makoto Yaguchi
 ; APPLICANT: Robert L. Campbell
 ; APPLICANT: David R. Rose
 ; TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Gowling, Strathy & Henderson
 ; STREET: Suite 2600, 160 Elgin Street
 ; CITY: Ottawa
 ; STATE: Ontario
 ; COUNTRY: Canada
 ; ZIP: K1P 1C3
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
 ; COMPUTER: IBM PC
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: WordPerfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/044.621D
 ; FILING DATE: April 8, 1993
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Judy A. Erratt
 ; REGISTRATION NUMBER: 34,076
 ; REFERENCE/DOCKET NUMBER: 08-863796
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 613-786-0199
 ; TELEFAX: 613-563-9869
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 27:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 190
 ; TYPE: Amino Acid
 ; STRANDEDNESS: No. 5405769 Relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; DESCRIPTION: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Trichoderma viride
 ; STRAIN: Trichoderma viride, 20kD
 ; IMMEDIATE SOURCE:
 ; POSITION IN GENOME:
 ; FEATURE:
 ; PUBLICATION INFORMATION:
 ; AUTHORS: Yaguchi M., Roy C., Ujile M., Watson
 ; AUTHORS: D.C., & Wakarchuk W.

; TITLE: Amino Acid Sequence of the Low-Molecular-
 ; TITLE: Weight Xylanase from Trichoderma viride
 ; JOURNAL: Xylans and Xylanases
 ; VOLUME:
 ; ISSUE:
 ; PAGES: 149-154
 ; DATE: 1992
 ; DOCUMENT NUMBER:
 ; FILING DATE:
 ; PUBLICATION DATE:
 ; RELEVANT RESIDUES IN SEQ ID NO:
 US-08-044-621D-27

Query Match 98.8%; Score 1032; DB 1; Length 190;
 Best Local Similarity 98.4%; Pred. No. 8.1e-89;
 Matches 187; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 QTIQPGTGYNNGYFYSYWNDGHHGVTYTNPGGQFQSVNMSNGNFVGGKMGQPGTKNKVI 60
 Db 1 QTIQPGTGFNNGYFYSYWNDGHHGVTYTNPGGQFQSVNMSNGNFVGGKMGQPGTKNKVI 60
 Qy 61 NFSGSYNPNNGSYLSVYGSWRNPLIEYIVENFGTYNPNSTGATKLGVTSDGSVYDIYRT 120
 Db 61 NFSGSYNPNNGSYLSVYGSWRNPLIEYIVENFGTYNPNSTGATKLGVTSDGSVYDIYRT 120
 Qy 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAWAQOGLTGLTMDYQIVAVEGYF 180
 Db 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAWAQOGLTGLTMDYQIVAVEGYF 180
 Qy 181 SSGSASITVS 190
 Db 181 SSGSASITVS 190

RESULT 8
 US-09-254-733-7
 ; Sequence 7, Application US/09254733
 ; Patent No. 6277596
 ; GENERAL INFORMATION:
 ; APPLICANT: WATANABE, MANABU
 ; APPLICANT: MORIYA, TATSUKI
 ; APPLICANT: AOYAGI, KAORI
 ; APPLICANT: SUMIDA, NAOMI
 ; APPLICANT: MURAKAMI, TAKESHI
 ; TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULOSE CBH1 GENES ORIGINATING
 ; TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR MASS-PRODUCING
 ; TITLE OF INVENTION: PROTEINS OR PEPTIDES THEREWITH
 ; FILE REFERENCE: 99-0266*/LC(WMC)/00144
 ; CURRENT APPLICATION NUMBER: US/09/254.733
 ; CURRENT FILING DATE: 1999-05-07
 ; NUMBER OF SEQ ID NOS: 52
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 223
 ; TYPE: PRT
 ; ORGANISM: TRICHODERMA VIRIDE MC300-1
 US-09-254-733-7

Query Match 97.2%; Score 1016; DB 4; Length 223;
 Best Local Similarity 96.8%; Pred. No. 3.1e-87;
 Matches 184; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 QTIQPGTGYNNGYFYSYWNDGHHGVTYTNPGGQFQSVNMSNGNFVGGKMGQPGTKNKVI 60
 Db 34 QTIQPGTGYNNGYFYSYWNDGHHGVTYTNPGGQFQSVNMSNGNFVGGKMGQPGTKNKVI 93
 Qy 61 NFSGSYNPNNGSYLSVYGSWRNPLIEYIVENFGTYNPNSTGATKLGVTSDGSVYDIYRT 120
 Db 94 NFSGSYNPNNGSYLSVYGSWRNPLIEYIVENFGTYNPNSTGATKLGVTSDGSVYDIYRT 153
 Qy 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAWAQOGLTGLTMDYQIVAVEGYF 180
 Db 154 QRVNPSIEGTFTFYQYWSVRNRHSSGSVNTANHFNAWAQOGLTGLTMDYQIVAVEGYF 213

QY 181 SSGSASITVS 190
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-28

Db 214 SSGSASITVS 223

RESULT 9
US-08-044-621D-28
; Sequence 28, Application US/08044621D
; Patent No. 5405769
; GENERAL INFORMATION:
; APPLICANT: Warren W. Wakarchuk
; APPLICANT: Wing L. Sung
; APPLICANT: Makoto Yaguchi
; APPLICANT: Robert L. Campbell
; APPLICANT: David R. Rose
; TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
; TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gowling, Strathly & Henderson
; STREET: Suite 2600, 160 Elgin Street
; CITY: Ottawa
; STATE: Ontario
; COUNTRY: Canada
; ZIP: K1P 1G3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 in., 360kB storage
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/044,621D
; FILING DATE: April 8, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Judy A. Erratt
; REGISTRATION NUMBER: 34,076
; REFERENCE/DOCKET NUMBER: 08-863796
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 613-786-0199
; TELEFAX: 613-563-9869
; TELEX:
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 190
; TYPE: Amino Acid
; STRANDEDNESS: No. 5405769 Relevant
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: NO
; ORIGINAL SOURCE:
; ORGANISM: Trichoderma harzianum,
; STRAIN: Trichoderma harzianum, 20kD
; IMMEDIATE SOURCE:
; POSITION IN GENOME:
; FEATURE:
; PUBLICATION INFORMATION:
; AUTHORS: Yaguchi M., Roy C., Watson D.C., Rollin
; AUTHORS: F., Tan L.U.L., Senior D.J., & Saddler
; AUTHORS: J.N.
; TITLE:
; JOURNAL: Xylans and Xylanases
; VOLUME:
; ISSUE:
; PAGES: 435-438
; DATE: 1992

QY 181 SSGSASITVS 190
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-28

Db 214 SSGSASITVS 223

RESULT 9
US-08-044-621D-28
; Sequence 28, Application US/08044621D
; Patent No. 5405769
; GENERAL INFORMATION:
; APPLICANT: Warren W. Wakarchuk
; APPLICANT: Wing L. Sung
; APPLICANT: Makoto Yaguchi
; APPLICANT: Robert L. Campbell
; APPLICANT: David R. Rose
; TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
; TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gowling, Strathly & Henderson
; STREET: Suite 2600, 160 Elgin Street
; CITY: Ottawa
; STATE: Ontario
; COUNTRY: Canada
; ZIP: K1P 1G3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 in., 360kB storage
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/044,621D
; FILING DATE: April 8, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Judy A. Erratt
; REGISTRATION NUMBER: 34,076
; REFERENCE/DOCKET NUMBER: 08-863796
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 613-786-0199
; TELEFAX: 613-563-9869
; TELEX:
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 190
; TYPE: Amino Acid
; STRANDEDNESS: No. 5405769 Relevant
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: NO
; ORIGINAL SOURCE:
; ORGANISM: Trichoderma harzianum,
; STRAIN: Trichoderma harzianum, 20kD
; IMMEDIATE SOURCE:
; POSITION IN GENOME:
; FEATURE:
; PUBLICATION INFORMATION:
; AUTHORS: Yaguchi M., Roy C., Watson D.C., Rollin
; AUTHORS: F., Tan L.U.L., Senior D.J., & Saddler
; AUTHORS: J.N.
; TITLE:
; JOURNAL: Xylans and Xylanases
; VOLUME:
; ISSUE:
; PAGES: 435-438
; DATE: 1992

ORGANISM: Trichoderma harzianum
PUBLICATION INFORMATION:
AUTHORS: Yaguchi, M
AUTHORS: Roy, C
AUTHORS: Watson, D. C.
AUTHORS: Rollin, F
AUTHORS: Tan, L. U. L.
AUTHORS: Senior, D. J.
AUTHORS: Saddler, J. N.
JOURNAL: Xylan and xylanase
PAGES: 435-438
DATE: 1992
US-08-709-912-14

Query Match 95.3%; Score 996; DB 1; Length 190;
Best Local Similarity 94.7%; Pred. No. 1.8e-85;
Matches 180; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 1 OTTQPTGTGNGYFYSYNDGCHGVYTYNGPGQFVSNNNSNGFVGGKQWPGTKNKVI 60
DB 1 QTICPGTGSNGYYSYNDGCHGVYTYNGGGSGFTVNNNSNGFVGGKQWPGTKNKVI 60
QY 61 NFSGSYNPGNSYLSVYSGSRNPLIEYIVENFGTNPSTGATKLGCVTSDGSVYDIYRT 120
DB 61 NFSGSYNPGNSYLSVYSGSRNPLIEYIVENFGTNPSTGATKLGCVTSDGSVYDIYRT 120
QY 121 QRYNQPSSIIGTATFYQYWSVRRNRHSSGVSNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180
DB 121 QRYNQPSSIIGTATFYQYWSVRRNRHSSGVSNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 11

US-09-047-370-14
Sequence 14, Application US/09047370
Patent No. 5866408
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of xylanase to improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma harzianum
PUBLICATION INFORMATION:
AUTHORS: Yaguchi, M
AUTHORS: Roy, C
AUTHORS: Watson, D. C.
AUTHORS: Rollin, F
AUTHORS: Tan, L. U. L.
AUTHORS: Senior, D. J.
AUTHORS: Saddler, J. N.
JOURNAL: Xylan and xylanase
PAGES: 435-438
DATE: 1992
US-09-047-370-14

Query Match 95.3%; Score 996; DB 2; Length 190;
Best Local Similarity 94.7%; Pred. No. 1.8e-85;
Matches 180; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 1 OTTQPTGTGNGYFYSYNDGCHGVYTYNGPGQFVSNNNSNGFVGGKQWPGTKNKVI 60
DB 1 QTICPGTGSNGYYSYNDGCHGVYTYNGGGSGFTVNNNSNGFVGGKQWPGTKNKVI 60
QY 61 NFSGSYNPGNSYLSVYSGSRNPLIEYIVENFGTNPSTGATKLGCVTSDGSVYDIYRT 120
DB 61 NFSGSYNPGNSYLSVYSGSRNPLIEYIVENFGTNPSTGATKLGCVTSDGSVYDIYRT 120
QY 121 QRYNQPSSIIGTATFYQYWSVRRNRHSSGVSNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180
DB 121 QRYNQPSSIIGTATFYQYWSVRRNRHSSGVSNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 12

US-08-768-373-2
Sequence 2, Application US/08768373
Patent No. 6228629
GENERAL INFORMATION:
APPLICANT: PALOHEIMO, MARJA
APPLICANT: HAKOLA, SATU
APPLICANT: M NYL, ARJA
APPLICANT: VEHMAANPER, JARI
APPLICANT: LANTTO, RAIJA
APPLICANT: LAHTINEN, TARJA
APPLICANT: FAGERSTR M, RICHARD
APPLICANT: SUOMINEN, PIIRKO
TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/768,373
;; FILING DATE: 17-DEC-1996
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/008,746
;; FILING DATE: 18-DEC-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/020,839
;; FILING DATE: 28-JUN-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CIMBALA, MICHELE A.
;; REGISTRATION NUMBER: 33,851
;; REFERENCE/DOCKET NUMBER: 1050.0540003
;; TELEPHONE: (202) 371-2600
;; TELEFAX: (202) 371-2540
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 261 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; ORIGINAL SOURCE:
;; ORGANISM: Chaetomium thermophilum
;; STRAIN: CBS730.95
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..261
;; OTHER INFORMATION: /label= XLNA
US-08-768-373-2

Query Match 69.0%; Score 721.5; DB 4; Length 261;
Best Local Similarity 65.8%; Pred. No. 1e-59; Mismatches 36; Indels 1; Gaps 1;
Matches 125; Conservative 28; Mismatches 36; Indels 1; Gaps 1;
QY 1 QTI-QPGTCYNGYFYSYVNDGHHGVTYNGPGQFSVNWNSGNGFVGGKQPGTKNKV 59
DB 27 QLTSSATGTHGYYSFTDGGNIRENLESGGYSVTWGNGNWVGKGNPGTDNRV 86
QY 60 INFSGSNNGNSYLSVGSNRNPLIEYIVENFGTYNPSTGATKLGVTSDGSVDIYR 119
DB 87 INTADYRNGNSYLAVGTWRNPLIEYIVESFGYDPTGATRGSVTDDGGTYNIYR 146
QY 120 TORVNQPSIGTATFYQYVSWVRNRHRSQSVNTANHFNAWAQOGLTGLTMDYQIVAVEGY 179
DB 147 TORVNAPSIEGTFYQYVSWVTSKRTGCTVTMANHFNAWRQAGLQGLSHDIQIVATEGY 206
QY 180 FSSGSASITV 189
DB 207 YSSGSATNVV 216

RESULT 13
US-08-290-979A-8
; Sequence 8, Application US/08290979A
; Patent No. 5610046
; GENERAL INFORMATION:
; APPLICANT: VAN OOLJEN, Albert J.H.
; APPLICANT: DE GRAAFF, Leendert H.
; APPLICANT: VAN DEN BROECK, Henriette C.
; APPLICANT: VISSER, Jacob
; TITLE OF INVENTION: Cloning and Expression of xylanase B
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006-1812

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/290,979A
;; FILING DATE: 22-SEP-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: KATE H. MORASHIGE
;; REGISTRATION NUMBER: 29,959
;; REFERENCE/DOCKET NUMBER: 4615-0045.00
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 887-1500
;; TELEFAX: (202) 887-0763
;; TELETYPE: 90-4030 MRSN FOERS WSH
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 225 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-290-979A-8
Query Match 63.7%; Score 665.5; DB 1; Length 225;
Best Local Similarity 65.6%; Pred. No. 1.4e-54;
Matches 120; Conservative 22; Mismatches 40; Indels 1; Gaps 1;
QY 7 TCYNNGYFYSYVNDGHHGVTYNGPGQFSVNWNSGNGFVGGKQPGTKNKVINPFGSY 66
DB 43 TGENNGFYYSFTDGGDVTYNGDAGSYTVEMSNVGNFVGGKGNPQSAQD-ITYSGTF 101
QY 67 NPNNGSYLSVGSNRNPLIEYIVENFGTYNPSTGATKLGVTSDGSVDIYRTORVNQ 126
DB 102 TFSGNGYLSVYGTWTDPLIEYIVESYGYDNGPGSGTYKGTVTSDGSVDIYRTATRNA 161
QY 127 SIIGTATFYQYVSWVRNRHRSQSVNTANHFNAWAQOGLTGLTMDYQIVAVEGYFSSGS 186
DB 162 SIQGTATFYQYVSWVRNQKRVGCTVTSNHFNAWAKLGMHLGTHNYQIVATEGYQSSGSS 221
QY 187 ITV 189
DB 222 ITV 224
RESULT 14
US-08-768-373-4
; Sequence 4, Application US/08768373
; Patent No. 6228629
; GENERAL INFORMATION:
; APPLICANT: PALOHEIMO, MARJA
; APPLICANT: HAKOLA, SATU
; APPLICANT: M NYL, ARJA
; APPLICANT: VEHMAANPER, JARI
; APPLICANT: LANTTO, RAIJA
; APPLICANT: LAHTINEN, TARJA
; APPLICANT: FAGERSTR M, RICHARD
; APPLICANT: SUOMINEN, PIIRKKO
; TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,
; AND USES THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/768, 373

FILING DATE: 17-DEC-1996

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/008, 746

FILING DATE: 18-DEC-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/020, 839

FILING DATE: 28-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: CIMBALA, MICHELE A.

REGISTRATION NUMBER: 33,851

REFERENCE/DOCKET NUMBER: 1050.0540003

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 230 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

ORGANISM: Chaetomium thermophilum

STRAIN: CBS730.95

FEATURE:

NAME/KEY: Protein

LOCATION: 1..230

OTHER INFORMATION: /label= XLNB

US-08-768-373-4

Query Match 62.88; Score 656.5; DB 4; Length 230;

Best Local Similarity 64.18; Pred. No. 9.6e-54;

Matches 118; Conservative 23; Mismatches 42; Indels 1; Gaps 1;

Qy 6 GTGYNNGYFYSYNDGHGGVYTTNGPGQFQSVNNSNGFNFGKGPQGTKNKVINFGSGS 65

Db 45 GTGTHNGWYYSFWDGGGTWYTTNGSGSYVNQNGFNFGKGPQGTKNKVINFGSGS 103

Qy .66 YNPNGNSYLSVYGSNRPLIEYIVENFGYNTPTGATKLGVTSDGSVDIYRTQVNO 125

Db 104 YNPGNSYLAITGTRNPLVEYIVESYGTYPDPSSGAQLGTFQSDGTYKIAKSTRYA 163

Qy 126 PSIIIGTATFYQWSVRRNHRSSGVSNTANHFNAWAQOGLTLGTMDYQIVAVEGYFSSGSA 185

Db 164 PSIEGKTFTQYWSVRSKRVGGTWTVANHFNAWKSGLNLGSHDYQIVAVEGYKSSGSA 223

Qy 186 SITV 189

Db 224 SITV 227

RESULT 15

US-08-886-765-2

Sequence 2, Application US/08886765

Patent No. 5817500

GENERAL INFORMATION:

APPLICANT: Hansen, Peter Kamp

APPLICANT: Wagner, Peter

APPLICANT: Mullertz, Anette

APPLICANT: Knap, Inge Helmer

TITLE OF INVENTION: Animal Feed Additives

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: NO. 58175000 No. 58175000disk of No. 58175000th America, Inc.

STREET: 405 Lexington Avenue

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10174

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA: US/08/886, 765

APPLICATION NUMBER: 435

FILING DATE: 1-JUL-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Lambiris, Elias J

REGISTRATION NUMBER: 33,728

REFERENCE/DOCKET NUMBER: 4324.204-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123

TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 225 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-886-765-2

Query Match 60.88; Score 635.5; DB 2; Length 225;

Best Local Similarity 60.28; Pred. No. 8.4e-52;

Matches 115; Conservative 28; Mismatches 47; Indels 1; Gaps 1;

Qy 1 QTIQPGTGYNNGYFYSYNDGHGGVYTTNGPGQFQSVNNSNGFNFGKGPQGTKNKVI 60

Db 32 QTPNSEGWHGYYYSWSDGGAQATYINLEGGTYEISWGGNLVGGKGNPGLNARAI 91

Qy 61 NFGSYNPNNGNSYLSVYGSNRNPLIEYIVENFGYNTPTGATKLGVTSDGSVDIYRT 120

Db 92 HFEQVYQPNNGNSYLSVYGSNRNPLIEYIVENFGYNTPTGATKLGVTSDGSVDIYRT 151

Qy 121 QRVNQPSIIIGTATFYQWSVRRNHRSSGVSNTANHFNAWAQOGLTL-GTMDYQIVAVEGY 179

Db 152 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDARAGLNVDGHDHYQIVAVEGY 211

Qy 180 FSSGSAITVS 190

Db 212 FSSGYARITVA 222

Search completed: May 9, 2003, 10:13:04

Job time : 31 secs

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)